GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

- protein search, using sw model OM protein

. March Run on:

2, 2006, 00:31:42 ; Search time 206.5 Seconds
(without alignments)
917.057 Million cell updates/sec

Title: Perfect score:

US-08-981-087B-1 2288 1 SYTNDKILLILYFNKLYKKIK......TSSNGCFWSFISKEHGWQEN 431 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 segs, 439378781 residues

Searched:

Total number of hits satisfying chosen parameters:

2443163

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 0B 0B Minimum | Maximum |

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp1980s:\* geneseqp1990s: geneseqp2000s: geneseqp2002s: geneseqp2001s: A\_Geneseq\_ Database

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaw09014 Imm	Aab04103 Bot	Aab04096 Bot
ΠD	1 2288 100.0 431 2 AAW09014	432 4 AAB04103	AAR04096
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Length	431		
Watch Length DB	100.0	2288 100.0	100
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по	Immunogen	Botulism	Botülism	Modified	DipT HN d	BONT/F-HC	BONT/F-HC	Modified	Modified	Modified	BONT/F-HC	C. botuli	A mangane	A mangane	C. botuli	BONT/F-HC	BONT/F-HC	Synthetic	Clostrid	Synthetic	Botuliam	Clostridi	Clostridi	Botulism
Description	Aaw09014	Aab04103	Aab04096	Aae07894	Aae35692	Aae35693	Aae35694	Aae07893	Aae07890	Aae07892	Aae35713	Aae07901	Aay93309	Aay93312	Aae07900	Aae35711	Aae35710	Aay77138	Aaw68399	Aay77137	Aab04094	Aaw68396	Aaw68395	Aab04095
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Ð	AAW09014	AAB04103	AAB04096	AAE07894	AAE35692	AAE35693	AAE35694	AAE07893	AAE07890	AAE07892	AAE35713	AAE07901	AAY93309	AAY93312	AAE07900	AAE35711	AAE35710	AAY77138	AAW68399	AAY77137	AAB04094	AAW68396	AAW68395	AAB04095
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Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.3	78.7	63.4	63.4	63.3	62.3	62.2
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AAE07898	ADZ69764	AAY93307	AAISSIO	AARSSUID	ADW11038	ADZ36018	ADZ60275	ADZ69730	ADZ69729	ADZ69831	AAB04088	AAR95008	AAW68389	AAY77134	AAW68391	AAR95009	AAW68390	AAB04089	AAB04090	AAY77140
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59.2	49.0	49.0	9.6	49.0	49.0	49.0	49.0	49.0	49.0	49.0	48.7	48.7	48.7	48.7	48.7	48.7	48.7	48.6	48.6	48.4
1355.5	1120.5	1120.5	1120.5	1120.5	1120.5	1120.5	1120.5	1120.5	1120.5	1120.5	1113.5	1113.5	1113.5	1113.5	1113.5	1113.5	1113.5	1111.5	1111.5	1106.5
25	26	27	28	53	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

## ALIGNMENTS

Immunogenic type F botulinum toxin heavy chain (aa848-1278). Clostridium botulinum; type F strain Langeland AAW09014 standard; protein; 431 AA Botulinum toxin; neurotoxin; (first entry) (revised) 17-OCT-2003 31-MAR-1997 AAW09014; AAW09014

BEST AVAILABLE COP

BoBT/F; immunogen; vaccine; botulism. 95GB-00011909. 27-DEC-1996. WO9641881-A1. 12-JUN-1996; 

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

12-JUN-1995;

Elmore MJ, Mauchline ML, Minton NP, Pasechnik VA;

WPI; 1997-065467/06. N-PSDB; AAT48100

Immunogenic type F botulinum toxin polypeptide(8) - allows recombinant vaccine prodn.

Claim 5; Page 16-17; 37pp; English.

A polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278) of a type F botulinum neurotoxin (BoNT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAW09015-17) lack the light chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin, making them useful for vaccine prodn. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-0CT-2003 to standardise OS field)

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AAB04096 standard; protein; 432
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       WPI; 2001-016048/02.
N-PSDB; AAA54499.
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                                                                SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                   1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                Length 431;
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                                   Indels
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                 100.0%; Score 2288; DB 2; 100.0%; Pred. No. 2.6e-167;
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                                  Mismatches
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990S-0133867P.
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990S-0133869P.
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Clostridium botulinum.
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                           Similarity
 Sequence 431 AA;
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                                   Matches 431;
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Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a cond then posttranslationally nicked, forming a dichain consisting of a clio kDa heavy chain and a 50 kDa light chain which remain linked by a clisulfide bond. Nucleic acide encoding the carboxy-terminal (HC) or amino the used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acide are expressible in a recombinant companisms such as Escherichia coli or pichia pastoris. The use of recombinant nucleic acide are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium.

Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acide can be derived from
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New nucleic acids encoding the carboxy- or amino-terminal portions of theavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine against botulism.
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100.0%; Score 2288; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 431; Conservative 0; Mismatches 0;
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                                                                                                                                                     Disclosure; Fig 18b; 73pp; English.
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SILKDFWGNYLLYNKRYYLLILLRTDKSITQNSNFLNINQQRGVYQKFNIFSNTRLYTGV
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07-APR-2000; 2000GB-00008658.
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Clostridium botulinum.
Chimeric.
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(first entry)
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01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding the carboxy- or amino-terminal portions of theavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                         Botulism; toxin; neurotoxin; heavy chain; recombinant expression;
                                                                                  recombinant vector; antigen; immune response; vaccine; bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Botulism toxin heavy chain C-terminal sequence (serotype F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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; Pred. No. 2.6e-167;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Middlebrook JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium botulinum serotypes A-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 9b; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uery match 100.0%;
Best Local Similarity 100.0%;
Matches 431; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0133869P.
99US-0133873P.
99US-0146192P.
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                                                                                                                                                                  Synthetic.
Clostridium botulinum.
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N-PSDB; AAA54490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                               12-MAY-2000;
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12-MAY-1999
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12-MAY-1999
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                                                                                                                  infection
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell, where the translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial cell, where the translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the transment of a disease state associated with neuronal useful for the polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for delivering therapeutic substances to neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
360
                                                                                                                                                             NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                                                                              361
                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                         EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified clostridial heavy chain fragment #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE07894 standard; protein; 645 AA
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Shone CC;

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Sutton JM,
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Matches
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                                                                                                                                                                                                                                                                                                      GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNBYTIIDCIRNNNSG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
(BoNT/F) with translocation domain of diphtheria neurotoxin. (Updated 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                     SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                    Gaps
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                                                                                                          Length 645;
                                                                                                                                               Indels
                                                                                                        Score 2288; DB 4;
Pred. No. 4.3e-167;
                                                                                                                                               0,
                                                                                                      DB 4;
                                                                                                                                                  0; Mismatches
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                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium diphtheriae.
Clostridium botulinum.
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                                                                                                                                                    Matches 431; Conservative
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Best Local Similarity
                                                                 Sequence 645 AA;
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; promoting or inhibiting and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells apoptosis, release of an inflammatory confidence from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular crafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and the comprising comprising corpusatorerium dispitcheriae diphtheria toxin translocation commissing Corynebacterium diphtheriae diphtheria toxin translocation commissing Corynebacterium diphtheriae diphtheria toxin translocation commissing Corynebacterium diphtheriae diphtheria toxin translocation commission in the seemplification of the invention.

CUDDIA PLIN domain) and botulinum type Preudotoxin from Clostridium could up the comprision of the invention.
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Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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; Pred. No. 4.3e-167;
0; Mismatches 0;
                                                                                                                             Example 12; Page 57-60; 130pp; English
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Best Local Similarity
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AAE35693 standard; protein; 657

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Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                   Apoptosis, therapy, inflammatory mediator, intracellular trafficking; infection, Prion disease, Alzheimer' disease, hypersecretion disorder; muscle spasm, CODP, bronchitis, chronic obstructive pulmonary disease; torricolis, blephorospasm, asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain;
                                                               BoNT/F-Hc-DipT HN domain-thrombin linker fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; Page 60-63; 130pp; English.
                                                                                                                                                                                                                                                                                                                 (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                            2001GB-00012687
                                                                                                                                                                                                                                                                       21-MAY-2002; 2002WO-GB002384
                                                                                                                                                                Corynebacterium diphtheriae.
Clostridium botulinum.
Unidentified.
                                                                                                                                               botulinum type F neurotoxin
                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 431; Conservative
                                                                                                                                                                                                                                                                                                                                         Sutton JM, Shone CC;
                                           (first
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-167247/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 657 AA;
                                                                                                                                                                                                                            40200296467-A2.
                                                                                                                                                                                                                                                                                            24-MAY-2001;
                                                                                                                                                                                                                                                  05-DEC-2002.
                                            17-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                      Chimeric.
                      AAE35693
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The present sequence is a fusion construct hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheriat toxin translocation domain (DipT-MY domain), botulinum type F neurotoxin binding domain (BoNY/F-Hc) from Clostridium botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a trarget cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells, killing cells, promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for intrafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for inhibiting secretion from cells. The invention is also were treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spagms such as blephorospasm, torticolis and including muscle spagms such as blephorospasm; torticolis and

Page 63-65; 130pp; English (MICR-) MICROBIOLOGICAL RES AUTHORITY 24-MAY-2001; 2001GB-00012687 Shone CC; WPI; 2003-167247/16. Example 12; Sutton JM, ; ; ô 286 9 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 227 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF Gaps 0; Length 657; Indels Score 2288; DB 6; Pred. No. 4.5e-167; ö 0; Mismatches 100.0%; 100.0%;

646 360 586 420 240 466 300 526 406 287 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG EVIIRKNGSTDISNTDNFVRKNDLAVINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 431 657 FISKEHGWQEN PISKEHGWOEN 181 407 241 467 527 361 421 647 121 301 원 g 원 ò 용 ò g 8 셤 ò 8 Š

AAE35694 standard; protein; 657 AAE35694

RESULT

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(first entry) 17-JUN-2003 BONT/F-Hc-DipT HN domain-factor Xa linker fusion construct.

muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain; Apoptosis, therapy, inflammatory mediator, intracellular trafficking, infection, Prion disease, Alzheimer' disease, hypersecretion disorder; botulinum type F neurotoxin

Corynebacterium diphtheriae. Clostridium botulinum. Clostridium b Unidentified.

Chimeric

WO200296467-A2.

05-DEC-2002.

21-MAY-2002; 2002WO-GB002384

Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.

The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for treatment selected from promoting or inhibiting survival of cells;

GIXSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANBYTIIDCIRNNNSG 120

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preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and hypersecretion disorders such as blephorospasm, torticolis and construct comprising Corymabacterium diphtheria toxin translocation commain (DipT-HN domain), botulinum type F neurotoxin binding domain (BoNT/F-HC) from Clostridium botulinum and factor Xa linker peptide. This sequence is used in the exemplification of the invention
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Sequence 657 AA;

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                                                                                                                       GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                         WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                                                                                                                                                                                                          526
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                                                                                                                                                                                                                                                                                                                                                                                                                                      420
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                                                                                                                                                                                                                  347 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 406
                                                                                                                                                                                                                                                                            NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 466
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                                                                            SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                           1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                                                                                                                                                                                             SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                              Gaps
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100.0%; Score 2288; DB 6; Length 657; 100.0%; Pred. No. 4.5e-167;
                              0; Indels
                             0; Mismatches
              Best Local Similarity 100.
Matches 431; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISKEHGWQEN 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587
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Query Match
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Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; botulinum neurotoxin type F; BONT/F.
                                                                                                                    Modified clostridial heavy chain-superoxide dismutase conjugate #5.
                             AAE07893'standard; protein; 685 AA
                                                                                                                                                                                                         Geobacillus stearothermophilus
                                                                                        (first entry)
                                                                                                                                                                                                                       Influenza virus.
Clostridium botulinum.
                                                                                        01-NOV-2001
                                                           AAE07893;
RESULT 8
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell, which comprises a binding domain capent into the neuronal cell, where the translocation domain is not a terminal half of HC, designated as HN), that translocates the therapeutic capent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are casful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the constructs are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from Bacillus stearothermophilus, linker that can be cleaved by factor Xa, translocation peptide from influence vius and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F) New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells. (MICR-) MICROBIOLOGICAL RES AUTHORITY. Example 9; Page 43; 50pp; English 04-DEC-2000; 2000WO-GB004644 02-DEC-1999; 99GB-00028530 07-APR-2000; 2000GB-00008658 Shone CC, Sutton JM, WPI; 2001-514643/56 Sequence 685 AA; WO200158936-A2 16-AUG-2001 Synthetic. Chimeric. 

Gaps ö Length 685; Indels Score 2288; DB 4; Pred. No. 4.7e-167; 0; Mismatches 100.0%; Best Local Similarity 100. Matches 431; Conservative Query Match

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EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 614

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EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocates the therapeutic capturint of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructs are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from Bacillus stearothermophilus, linker that can be cleaved by factor Xa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
NSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                   615 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 674
                                                                                                                                                                                                                                                                                                                       Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphtheria neurotoxin and a neuronal cell-
com botulinum neurotoxin type F (BoNT/F)
                                                                                                                                                                                                                                                                                       Modified clostridial heavy chain-superoxide dismutase conjugate #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific binding domain from botulinum neurotoxin type F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                     AAE07890 standard; protein; 862 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                           Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
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                                                                  431
                                                                                           FISKEHGWQEN 685
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                                                                  FISKEHGWOEN
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DB 4';

100.0%; Score 2288;

Query Match

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                                                                                                                                                           121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                                         61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYPNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                         GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANNEYTIIDCIRNNNSG 551
                                                                          491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                  192 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGELGFHSNNLVASSWYNNIRKNTSSNGCFWS
                                                                                                                                                                                                                                                                        241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                                                                                                                                EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
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                                                                     SYTNDKILILYFUKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                   181 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                               1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified clostridial heavy chain-superoxide dismutase conjugate #4.
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        Pred. No. 6.3e-167;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE07892 standard; protein; 887 AA
100.08; PI
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Corynebacterium diphtheriae.
Clostridium botulinum.
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07-APR-2000; 2000GB-00008658.
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          Best Local Similarity 100.
Matches 431; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514643/56
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                                                                                                                                  492
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BONT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN chain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for the treatment of a disease state of the invention are calle including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate compuses a mitochondrial leader sequence from human Mn-conjugate comprises a mitochondrial leader sequence from human merotoxin and a neuronal cell-specific binding domain from chiptheria neurotoxin and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F)
New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                           English
                                                                                                                           42; 50pp;
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ô Query Match
100.0%; Score 2288; DB 4; Length 887;
Best Local Similarity 100.0%; Pred. No. 6.5e-167;
Matches 431; Conservative 0; Mismatches 0; Indels 0 Sequence 887 AA;

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Gaps

SYTNDKILLILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 516 GIYSSKRSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANBYTIIDCIRNNNSG 576 240 756 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP SILKDFWGNYLLYNKRYYLLNLERTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 431 887 FISKEHGWOEN FISKEHGWOEN 697 457 181 637 757 817 121 241 301 517 361 421 877 19 요 ઠે g g ઠ 셤 ò Q 8 셤 ठ 셤 ò à

WKISLAYNKIIWTLODTAGNNOKLVFNYTOMISISDYINKWIFVTITNNRLGNSRIYING 180

609 121

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979 AA.

AAE35713 standard; protein;

RESULT 11

(first entry)

17-JUN-2003

AAE35713;

RXXXEX

The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a targets the effector protein to a tradect call. The card composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells.

The preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection, do in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking for modulating expression of cell-surface markers and for thibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer disease and wide range of disorders including muscle spasms such as blephorospasm, torticals and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HM domain), botulinum type F neurotoxin binding domain (BONT/F-HC) from Clostridium botulinum and factor Xa linker peptide and Yersinia pestis targetted effector protien YopT. This sequence is used in the exemplification of the invention 608 120 Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell. 09 Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spaem; COPD; Pronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain; botulinum type F neurotoxin; targetted effector protien; YopT. SYINDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYTYSTNRNQF GIYSSKESEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF Gaps ö Length 979; Indels Score 2288; DB 6; Pred. No. 7.4e-167; 0; Mismatches 0; Example 12; Page 110-114; 130pp; English. (MICR-) MICROBIOLOGICAL RES AUTHORITY. 100.0%; 100.0%; 24-MAY-2001; 2001GB-00012687 21-MAY-2002; 2002WO-GB002384 Corynebacterium diphtheriae. Clostridium botulinum. Matches 431; Conservative Shone CC; WPI; 2003-167247/16 Query Match Best Local Similarity Yersinia pestis. Sequence 979 AA; WO200296467-A2 Unidentified. 05-DEC-2002 Sutton JM, 549 61 Chimeric g ઠે ઠ

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05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                  909 NSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 968
                                                                                                      SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 848
                                                                                                                                EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
                                                                                                                                                       EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 908
                                                                                                                                                                                 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 728
                                                                                                                                                                                                                                                                                                                                                                                                                                         stroke; epilepsy;
                                          NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                            NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                               SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                                                                                                                                                                                                               botulinum C2 translocation domain with BoNT/F-binding domain #2.
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                                                                                                                                                                                                                                                                                                                                   AAE07901 standard; protein; 1032 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000; 2000WO-GB004644
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962 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYNNIRKNTSSNGCFWS 1021
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is C. botulinum C2 enterotoxin translocation domain with botulinum neurotoxin type F (BoNT/F) binding domain used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                                                                                                                                                                                                                 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
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                                                                                                                                                                                                                                       1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                              Length 1032;
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                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A manganese superoxide dismutase (Mn-SOD) construct
                                                                                                                                         100.0%; Score 2288; DB 4;
100.0%; Pred. No. 7.9e-167;
                                                                                                                                                                                               0; Mismatches
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Clostridium botulinum.
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                                                                                                                                                                            Best Local Similarity 100.
Matches 431; Conservative
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                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                       Sequence 1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200028041-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                  The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and motor neurone diseases
                                                           cleavable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFININQQRGYYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                      Novel composition, comprising superoxide dismutase linked by a clear linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
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                                                                                                                                                                                                                                                                                                                                                                                         Length 1059;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2288; DB 3;
100.0%; Pred. No. 8.2e-167;
tive 0; Mismatches 0;
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Silman
                                                                                                                         Disclosure; Page 48-51; 65pp; English
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Hallis B,
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Sutton JM,
                             WPI; 2000-376553/32
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                Sequence 1059 AA;
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ပ္ပဲ
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Best Local S
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The present sequence represents a construct of the invention, comprising a mitochondrial leader sequence from human manganese superoxide dismutase (Mn-SOD), a Bacillus stearchtermophilus Mn-SOD, a linker that can be cleaved by thrombin and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
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              Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1084;
neuronal cell targeting component; NCTC; neuronal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 2288; DB 3;
; Pred. No. 8.4e-167;
0; Mismatches 0;
               oxidative stress; ischemic stroke; trauma; P
Huntington's disease; motor neurone disease;
botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                         ż
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                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 57-60; 65pp; English
                                                                                                  Homo sapiens.
Geobacillus stearothermophilus.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Best Local Similarity 100.
Matches 431; Conservative
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                                                                                                                                                                                                                                                                                                                                           Sutton JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1084 AA;
                                                                                                                                                                       WO200028041-A1
                                                                                                                                                                                                                                      35-NOV-1999;
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial continuance in the invention are a wife domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for treat disorders of the cubiculing neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum
                    1014 NSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
                                                                                                                                                                                                                                                                                                                                     Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                       C2 translocation domain with BoNT/F-binding domain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                               AAE07900 standard; protein; 1092 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 47; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2000; 2000WO-GB004644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1999; 99GB-00028530
07-APR-2000; 2000GB-00008658
                                                                                                                                                                                                                                                                      (first entry)
                                                                                         |||||||||||
1074 FISKEHGWQEN 1084
                                                                     421 FISKEHGWQEN 431
                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium botulinum
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                                                                                                                                                                                                                                                                                                       C. botulinum
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Length 1092; Indels 9

662 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 721

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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF

Query Match 100.0%; Score 2288; DB 4; Best Local Similarity 100.0%; Pred. No. 8.5e-167; Matches 431; Conservative 0; Mismatches. 0;

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1081
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                                                                                NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
                                                                                                                                      SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV 300
GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 781
                            180
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                                                                                                902 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
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                                                                                                                                                                                                                                                  NSLGQ11VMDS1GNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
                             WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING
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                                                                                                                                                                                                                                                                                                                                   FISKEHGWQEN 1092
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Job time: 209.5 secs
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model 8 using protein search, protein 2, 2006, 00:39:17 ; Search time 36 Seconds
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1151.928 Million cell updates/sec March Run on:

US-08-981-087B-1 2288 1 SYTNDKILILYFNKLYKKIK.....TSSNGCFWSFISKEHGWQEN Title: Perfect score: Sequence:

431

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

of hits satisfying chosen parameters: Total number

residues

283416 segs, 96216763

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		,			COLUMNICO	
Result		Ouerv				
NO O	Score	Match	Length	80	QI .	Description
-	1833	80.1	1274	7	140813	neurotoxin type F
8	1827	79.9	1268	7	833411	botulinum neurotox
e	1457.5	63.7	1252	~	S21178	botulinum neurotox
4	1426	62.3	1251	7	JH0256	botulinum neurotox
Ŋ	1120.5	49.0	1296	Н	BTCLAB	bontoxilysin (EC 3
9	1092.5	47.7	1296	~	I40645	botulinum neurotox
7	816	35.7	366	7	S48110	neurotoxin type F
80	781	34.1	1291	7	140631	ı
σ	169	33.6	1291	-	A48940	bontoxilysin (EC 3
10	736.5	32.2	1297	~	839791	neurotoxin - Clost
11	645.5	28.2	369	7	S48109	neurotoxin type F
12	590.5	25.8	367	7	S48106.	neurotoxin type E
13	580.5	25.4	1276	7	811455	botulinum neurotox
14	553	24.2	1315	Н	BICLIN	tentoxilysin (EC 3
15	546	23.9	1291	N	A49777	botulinum neurotox
16	546	23.9	1291	~	S46431	botulinum neurotox
17	508	22.2	1285	~	870582	botulinum neurotox
18	267	н	1162	7	140817	botulinum toxin no
19	260	11.4	1162	7	A47708	progenitor toxin n
20	259	11.3	1193	7	868218	botulinum neurotox
21	244	10.7	1193	7	JC4901	nontoxic-nonhemagg
22	225.5		1196	~	JQ1467	toxin, nontoxic co
23	225.5	9.6	1196	7	S46430	botulinum neurotox
24	208.5		1165	~	I40644	botulinum neurotox
25	201	8.8		~	A53878 ·	ب
26	190	8.3	1844	(1	D71612	hypothetical prote
27	172.5	7.5	2136	N	A05037	
28	169	7.4	4688	N	F82885	prot
29	165.5	7.2	096	N	S72284	DNA-directed RNA p

hypothetical prote	UNA-directed KNA p	hypothetical prote	hypothetical prote	hypothetical prote	DNA-directed RNA p	hypothetical prote	ATP-dependent Clp	hypothetical prote	protein with 5'-3'	toxin-like outer m					
T18501	A45597	D71618	T18440	T18469	RNZQBF	A71661	B71612	B71605	T18460	B90590	E71616 .	872278	C64474	A71621	B64596
0	~	~	N	~	-	7	7	~	~	N	7	N	~	0	7
3394	2339	1436	4550	786	1024	588	3973	807	836	640	1247	765	2894	1188	1943
7.2	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.8
164	163	162.5	162.5	161.5	161.5	160	160	159.5	159.5	159	158	157.5	157.5	157	156.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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neurotoxin type F - Clostridium botulinum C;Species: Clostridium botulinum

Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C;Accession: I40813; S48108
R;East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.E Fers Microbiol. Lett. 96, 225-230, 1992
A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A;Reference number: I40644

A;Accession: 140813 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecules: 1-1274 <RES> A;Cross-references: UNIPROT:P30996; UNIPARC:UPI0000126B8A; GB:M92906; NID:g144866; PIDN:

R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48108
A;Status: preliminary; translation not shown

A;Molecule type: DNA \*Residues: 634-1002 <CAM> A;Cross-references: UNIPARC:UPI000016EA7B; EMBL:X70816; NID:g407788; PIDN:CAAS0147.1; PI C;Superfamily: tetanus toxin

C, Keywords: neurotoxin

8; Gaps Length 1274; Query Match

80.1%; Score 1833; DB 2; Length 1
Best Local Similarity 81.3%; Pred. No. 8.4e-98;
Matches 352; Conservative 33; Mismatches 40; Indels

906 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIXSTNRNQF рp ઠે

120

996 WKISLNYNK---IIWTLQDTAGNNQKLVPNYTQMISISDYINKWIFVTITNNRLGNSRIY 177 셤

61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG

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121 ઠે 엄

1086 237 178 INGNLIDEKSISNLGDIHVSDNILPKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDE 1027 INGNLIVEKSISNLGDIHVSDNILFKIVGCDDETYVGIRYFKVFNTELDKTEITLYSNE ઠ g

PDPSILKDFWGNYLLYNKRYYLLINLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLY 238 à

셤

TGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTS 357 298

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A; Reduces: 616-982 < CAM>
A; Cross-references: UNIPARC:UPI00000BC6F0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; P. A; Cross-references: UNIPARC:UPI00000BC6F0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; P. A; Cross-references: UNIPARC:UPI00000BC6F0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; P. A; Cross-reference: D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem. Biophys. Res. Commun. 183, 107-113, 1992
A; Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum typ: A; Reference number: JH0255; MUD:92181428; PMID:1543481
A; Accession: JH0257
A; Accession: JH0257
A; Accession: JH0257
A; Residues: 1-176, R; 178-197, C', 199-339, R', 341-772, 'I', 774-962, 'FE', 965-966, 'R', 968-: A; Cross-references: UNIPARC:UPI000016EA7F; EMBL:X62089; NID:940393; PIDN:CAA43999.1; PII A; Experimental source: strain Beluga
R; Biio. Chem. 265, 9153-9158, 1990
A; Title: The complete sequence of botulinum neurotoxin type A and comparison with other A; Reference number: A35294; MUD:90264400; PMID:2160960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Reldues: 1-176,'R', 178-252 < BIN>
A;Residues: 1-176,'R', 178-252 < BIN>
A;Cross-references: UNIPARC:UPI000017670F
A;Experimental source: strain Beluga
R;Gimenez, J.A.; DasGupta, B.R.
B;Giminie 72, 213-217, 1990
A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the 8:
A;Reference number: A60027; MUID:90344918; PMID:2116911
A;Accession: A60027
                                                                  neurotoxi
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                                                                                                                                                                                               EMBL: X62683;
                                                                                                                                                                                                                                                                          neurotoxin gene and specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           949 GWKVSLNHNEIIWTLODNAGINOKLAFNYGNANGISDYINKWIFVTITNDRLGDSKLYIN 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888
     R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P. Bur. J. Biochem. 204, 637-667, 1992
A;Title: The complete amino acid acquence of the Clostridium botulinum type-E
A;Fitles number: S21178; MUID:92114922; PMID:1541280
                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1252 * WHES
A; Residues: 1-1252 * WHES
A; Residues: 1-1252 * WHES
A; Casidues: 1-1252 * WHES
A; Campbell, K.D.; Collins, M.D.; Bast, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A; Title: Gene probes for identification of the botulinal neurotoxin gene and s A; Reference number: S48103; MUID:94013372; PMID:8408542
A; Accession: S48107
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA ****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNEYTIIDCIRNNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.7%; Score 1457.5; DB 2; Length 1252; 63.4%; Pred. No. 3.2e-76; tive 72; Mismatches 70; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 420-427 <GIM>
A,Cross-references: UNIPARC:UPI0000176710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276; Conservative
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                                                                                                               A; Accession: S21178
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botulinum neurotoxin type F - Clostridium barati

botulinum neurotoxin type F - Clostridium barati

c)speciaes Clostridium barati

c)speciaes Clostridium barati

c)Accession: 833411, 831860

R; Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.

FERS Microbiol. Lett. 108, 175-182, 1993

A; Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin

A; Reference number: 833411, MUD: 93252228; PMID: 8486245

A; Reference number: B33411

A; Residues: DNA

A; Residues: 1-1268 < THO>

A; Residues: 1-1268 < THO>

A; Residues: 1-1268 < THO>

C; Superfamily: tetanus toxin

C; Keywords: neurotoxin
                                                                                                                  960 KISLNYNNIIMTLQDTTGNNQKLVENYTQMIDISDYINKWTEVTITNNRLGHSKLYINGN 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
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botulinum neurotoxin type E precursor - Clostridium botulinum
C;Species: Clostridium botulinum botulinum c;Species: Clostridium botulinum c;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 31-Dec-2004
C;Accession: S21178; S48107; ŪH0257; B35294; A60027; S18111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYSSRLSEVNITQNNTIIYNSRYQNFSVSF#VRIPKYNNLKNLLNNEYTIINCMRNNNSG#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN
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                                                                                   NSNNSLGQ11VMDS1GNNCTMNFQNNNGGN1G1LGFHSNNLVASSWYYNN1RKNTSSNGC
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                                                                                                                                                                                                                                      FWSSISKENGWKE 1274
                                                                                                                                                                                       FWSFISKEHGWQE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 78.89
18; Conservative
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Matches 338;
                                                                                                                                                                                          418
                                                                                                                                     1202
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A; Residues: 1-1296 (SIN)>
A; Residues: 1-1296 (SIN)>
A; Cross-references: UNIPROT: P10845; UNIPARC: UP10000001386; GB:M30196; NID: g144864; PIDN: A; Cross-references: UNIPROT: P1084, subtype A
B; Cross-reference: strain 62A, subtype A
B; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
B; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin A; Reference number: S09492; MUID:90235864; PMID:2185020
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A;Residues: 1,'Q',3-26,'V',28-1296 <THO>
A;Cross-references: UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID
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R; Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A; Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A; Reference number: .867988; MUID: 96096783; PMID: 8521962
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R;Betley, M.J.; Somers, E.; DasGupta, B.R.
Bachem. Biophys. Res. Commun. 152, 1388-1395, 1989
A;Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-term A;Reference number: A33401; MUID:89350959; PMID:2669749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after extracted trom NCBI backbone (NCBIP:139159); sequence extracted from NCBI backbone (NCBIP:139159); sequence extracted m.L. Biochimie 72, 661-664, 1990
A;Title: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and aron acids at the N-terminus and A-title acids acids acids acids acids at the N-terminus and A-title acids a
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N;Alternate names: botulinum neurotoxin type A
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A35294; 809492; $68220; A33401; A53884; A60\(\overline{0}\)E; A27000
R;Binz, T; Kurazono, H; Wille, M; Frevert, J; Wernars, K.; Niemann, H.
J:Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with
A;Reference number: A35294; MUID:90264400; PMID:2160960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72, 45,
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240 PSILKDFWGNYLLYNKRYYLLMLLRTDKSITQNS-NFLNINQQRGVYQKPNIFSNTRLYT
                                                                                                                                                                                                                                                                                                                    TSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSN
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A;Residues: 867-880;1148-1217,'Y',1219 <GIM>
A;Cross-references: UNIPARC:UPI00000BBB24; UNIPARC:UPI0000173656
                                              A;Cross-rererence.
R;Gimenez, J.A.; DasGupta, B.R.
J. Protein Chem. 12, 351-363, 1993
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Residues: 1-12 <FUJ>
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A; Residues: 1-35 <BET>
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C; Species: Clostridium Dutyricum
C; Accession: J40256; S16145
R; Poulet, S:, Hauser, D:, Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem: BioChyp. Res. Commun. 133, 107-113, 1992
A; Fitle: Sequences of the botulinal neurocoxin E derived from Clostridium botulinum type
A; Reference number: J40256; MUID: 92181428; PMID: 1543481
A; Reference number: J40256; MUID: 92181428; PMID: 1543481
A; Residues: 1-27, E', 29-1251 cPUV
A; Residues: 1-27, E', 29-1251 cPUV
A; Residues: 1-27, E', 29-1251 cPUV
A; Repaidues: 1-27, E', 29-1251 cPUV
A; Rightian, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N.
A; Reference number: S16145; MUID: 91237316; PMID: 203376
A; Fitle: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxi
A; Fresidues: 1-229, 'W', 231-252 cFUUS
A; Researches: UNIPARC: UPT000016EA8F; EMBL: X53180; NID: 940407; PIDN: CAA37321.1; PID
A; Researches: Preliminary
A; Researches: UNIPARC: UPT000016EA8F; EMBL: X53180; NID: 940407; PIDN: CAA37321.1; PID
A; Researches: The heavy chain mediates the binding of toxin to cell receptors while the light Comment: The clostridial neurotoxins are toxins that inhibit neurotors while the light C; Superfamily: tetarius toxin
C; Reywords: neurotoxin
C; Reywords: Potulinum neurotoxin
C; Reywords: Potulinum perproxin
C; Reywords: Putle Public 
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                1009 GNLIDQKSILNLGNIHVSDNILFKIVNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPN 1068
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                                                                                            PSILKDFWGNYLLYNKRYYLLNLLRTDKSI-TQNSNFLNINQQRGVYQKPNIFSNTRLYT 298
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larity 62.8%; Pred. No. 2e-74;
Conservative 73; Mismatches 71; Indels 18
                                                                                                                                       GCFWSFISKEHGWQE 430
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Matches 273; Conserv
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Res. Microbiol. 144, 547-556, 1993

Res. Microbiol. 144, 547-556, 1993

A,Title: Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A, A,Rcestence number: 140645; MUID:94143603; PMID:8310180

A,Rcference number: 140645; MUID:94143603; PMID:8310180

A,Rcstus: preliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-1296

A,Residues: 1-1296
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A;Residues: 1-366 <CAM>
A;Cross-references: UNIPROT:Q57236; UNIPARC:UPI000016EA7C; EMBL:X70821; NID:g407792;
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S48110
J; Clin. Microbiol. 31, 2255-2262, 1993
A;Fitle: Gene probes for identification of the botulinal neurotoxin gene and the facession: S48110
A;Accession: S48110
A;Status: preliminary; translation not shown
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48.6%; Pred. No. 3.2e-55;
tive 76; Mismatches 133;
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Best Local Similarity
Matches 153; Conserv
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Best Local Similarity
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A; Residues: 2-47 chas2>
A; Cross-references: UNIPARC:UDI0000173659
A; Cross-references: UNIPARC:UDI0000173659
A; Cross-references: UNIPARC:UDI0000173659
A; Cross-references: UNIPARC:UDI0000173659
A; Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
J; Biol. Chem. 269, 1617-1620, 1994
A; Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A; Reference number: A49708; MUID:94124495; PMID:8294407
A; Contents: annotation
C; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synapt C; Genetics:
A; Gene: atx; botA
C; Function:
A; Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate C; Superfamily: tetanus toxin
C; Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot C; Superfamily: tetanus toxin
C; Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot C; Superfamily: tetanus toxin
C; Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot F; 2-444/Product: bontoxilysin A heavy chain #status experimental <HVX>
F; 245-1296/Product: bontoxilysin A heavy chain #status experimental <HVX>
F; 222/Afctive site: Glu #status predicted
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botulinum neurotoxin type A - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: L1-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40645
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               A,Reference number: A60025; MUID:91120847; PMID:2126206
A,Accession: A60025
A,Accession: Drotein
A,Molecule type: protein
A,Residues: 2-6;445-453, 'X', 455-457 <DASI>
A,Cross-references: UNIPARC:UP10000173657; UNIPARC:UP10000173658
B,Cross-references: UNIPARC:UP10000173658
A,Cross-references: UNIPARC:UP10000173658
A,Title: Partial sequence of the light chain of botulinum neurotoxin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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49.0%; Score 1120.5; DB 1;
Best Local Similarity 49.4%; Pred. No. 7.8e-57;
Matches 219; Conservative 78; Mismatches 127;
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q	214 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 273	OY 237 EPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSI <sup>2</sup> TQNSNFLNIN 279
& 43	61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANNEYTIIDCIRNNNSG 120 	TAKEYYMFINAGNKNSYIKLVKÖSSVGEILIRSKYNÖNSNY YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVE
<i>&amp;</i> ₽	121 WKISLNYNKIIWTLQDTAGNNQKLVPNYTQMIS 153 	Db 1138NLYIGEKFIIRRESNSQSIN-DDIVRKEDYIHLDLYLHHEEWRYY 1181  Qy 340 ADISIAKPEKIIKLIRTSNSNNSLGQIIVMDSIGNNCTWNFQNNNGGNIGLIGFH 394
RESULT 140631 non-pro C;Speci C;Date:	RESULT 8 140631 non-proteclytic botulinum neurotoxin type B precursor - Clostridium botulinum C.Species: Clostridium botulinum C.Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004	395SINILVASSWYYNNI-RKYTSSN-GCRGFISKTERKHGWGE 430 1242 RFYESGVLRKKYKDYFCISKWYLKEVKRKFYKSNLGCNWQFIPKDEGWTE 1291
C, Accel R, Hutsc Curr. A A, Title A, Refer A, Acce	C; Accession: 140631; S48103; S48104; S36015 R; Hutson, R.A.; Collins, M.D.; East, A.K.; Thompson, D.E. A; Trick: Microbiol. 28, 101-110, 1994 A; Ttele: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinu A; Reference number: 140631; MUD: 94122659; PMID: 7764370 A; Accession: 140631	RESULT 9 A48940 bontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum N,Alternate names: botulinum neurotoxin type B (BoNT/B) C;Species: Clostridium botulinum C;Species: Clostridium botus namision 18.80xx-1964 #toxt change 09.701-2004
A; Statu A; Molec A; Resid A; Cross	Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: DNA Residues: 1-1291 «RES> Cross-references: UNIPROT: QDBQ77; UNIPARC: UP100000BDC86; EMBL: X71343; NID: g296148; PIC	CiAccession: A48940; S44105; S21575; A4871; S0155; S08562; S0128; S08573; S08574 R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P. Appl. Environ. Microbiol. 58, 2345-2354, 1992 Appl. Environ. Microbiol. 58, 2345-2354, Man botulinum structural gene encoding the typ
J. Clir A;Title A;Refe		A, Reference number: A48940, MUID:92384550; PMID:1514783 A, Accession: A48940 A, Status: preliminary
A; Acces A; Statu A; Molec	Accession: S48103 Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA	A; Molecule type: DNA A; Residues: 1-1291 <whe> A; Cross-references: UNIPARC: UPI000016EA76; GB:M81186; NID:9144734; PIDN:</whe>
A;Residues: 63 A;Cross-refere A;Experimental A;Note: the nu	Residues: 634-761, 78', 763-841, M', 843, Tr', 845, 7M', 847-594 «CAM1»  Cross-references: UNIPARC:UPIONOUGBABER; EMBL:X70814; NID:9407778; PIDN:CAA50145.1; PI Experimental source: non-proteolytic strain 21298 (Scott) Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993	080, NCBIP:112081); this publi
A; Acce A; Stati	Accession: S48104 Status: preliminary Molecule troe: DNA	A.Title: Gene probes for identification of the botulinal neurotoxin gene and specific 1d A;Reference number: S48103; MUID:94013372; PMID:8408542 A;Accession: S48105
A; Resi-	A,Reaidues: 634-843, 'T', 845,'N', 847-994 «CAM2» A)Reaidues: 634-843, 'T', 845,'N', 847-994 «CAM2» A)Reprimental source: non-protecolytic strain Eklund 2B (Colworth 229) A)Experimental source: non-protecolytic strain Eklund 2B (Colworth 229) C, Comment: Rothlinn non-protecol in these strains may posses a capable catalytic strains.	A;Status: preliminary A;Molecule type: DNA A;Residues: 634-994 <cam> A;Cross-references: UNIPARC:UPI000016EA7A; EMBL:X70817; NID:9407782; PIDN:CAA50148.1; PI</cam>
C; Genet	C;Genetics: C;Gene	273
C; Keyw F; 2-44 F; 242-	C.; Neywords: metalloprotein; neurotoxin; transmembrane protein; zinc C; Neywords: metalloprotein; neurotoxin type B light chain #status predicted <lght> F; 2-441/Product: botulinum neurotoxin type B heavy chain #status predicted <hvy> F; 230, 234/Binding site: zinc (His) #status predicted</hvy></lght>	A, Description: Partial amino acid sequence of botulinum neurotoxin type B and comparisio A, Reference number: 821875 A, Accession: 821575 A, Molecule type: DNA
F;231/Ac Query Best	F;231/Active site: Glu #status predicted Query Match 34.1%; Score 781; DB 2; Length 1291; Best Local Similarity 37.0%: Pred. No. 2.5e-37;	PIDN:CAA77991.1; P stein, O.; Wernars,
Matches	nes 174; Conservative 9 1 SYTNDKILILYFNKLYKKI	A, Title: Minimal essential domains specifying toxicity of the light chains of tetanus to A, Reference number: A42871; MUD:92340509; PMID:1634516 A, Accession: A42871
qq		A.Status: nucleic acid sequence not shown A.Molecule type: mRM, 315-451 <kur> A.Residues: 1-313, 'S', 315-451 <kur></kur></kur>
ò a	61 GIYSSKPSEVNIAQNNDIIYNGRYQNPSISFWVRIPKYFNKVNLNNEYTIIDCIRNN 117 	A;Cross-references: UNIPARC:UP100000B3742 A;Experimental source: strain Okra A;Note: sequence extracted from NCBI backbone (NCBIP:109365)
& a	118 NSGWKISLMYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIY 177	Apparature 70, 811-817, 1988 AjTitle: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with A;Reference number: S07155; MUID:89000987; PMID:3139097
6 G	178 INGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSD 236	A;Accession: SV.13-8 A;Molecule type: protein A;Residues: 2-29,'M',31-45 <das> A;Cross-references: UNIPARC:UPI0000173650 A;Accession: S08562</das>

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C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S39791
K;Campbelly, K; Collins, M.D.; East, A.K.
Biochim. Biophys. Acta 1216, 487-491, 1993
A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium A;Reference number: S39791; MUID:94092745; PMID:8268233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 11297 < CCAM>
A;Cross-references: UNIPARC:UPI0000176706; EMBL:X74162; NID:g441275; PIDN:CAA52275.1; C;Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P30996; UNIPARC:UPI000016EA7B; EMBL:X70820; NID:g407790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTOLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDYGYVWD 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 PDPSILKDFWGNYLLYNKRYYLLN-----LLRTDKSITQNSNFLNINQQRGVYQKPN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 IFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVD-RDVEYRLYADISIAKPE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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C;Species: Clostridium botulinum
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
D;Date: 12-Feb-1998 #text_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN
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A;Residues: 1-369 <CAM>
1243 FYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 736.5; DB 2;
; Pred. No. 9.2e-35;
76; Mismatches 179;
                                                                                                                                                         neurotoxin - Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.7%;
Matches 164; Conservative 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: ccc....
C; Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: S39791
A,Status: preliminary
A,Molecule type: DNA
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A;Contents: annotation
C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
C;Genetics:
A;Gene: bont/b
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: S08574
A, Status: preliminary
A, Molecule type: protein
A, Molecule type: protein
A, Residues: 442-459 < SCH3>
A, Cross-references: UNIPARC: UPI0000173652
A, Schikavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.F.
Nature 359, 832-835, 1992
A, Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2 C, Superfamily: tetanus toxin C; Superfamily: tetanus toxin C; Keywords: hydrolase; metalloproteinse; neurotoxin; transmembrane protein; zinc C; Keywords: hydrolase; metalloproteinim #status experimental cLGHT> F; 442-1291/Product: bontoxilysin B heavy chain #status experimental cHVY> F; 230, 234/Binding site: zinc (His) #status predicted F; 231/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRD 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKYPKKEEEKLFLAPISDSDEFYNTIQIKEYDBQPTYSCQLLFKKDEESTDEIGLIGIHR 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYI 178
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                                                                                                                Arch. Biochem. Biophys. 238, 544-548, 1985.
A,Title: Partial amino acid sequences of botulinum neurotoxins A,Reference number: S07128; MUD:85197963; PMID:3888113
A,Resession: S07128
A,Status: preliminary
A,Molecule type: protein
A,Residues: 2-16 <SCH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 769; DB 1; Length 12 llarity 36.0%; Pred. No. 1.2e-36; Conservative 88; Mismatches 152; Indels
                                                                                                    В.К
         A;Molecule type: protein
A;Residues: 442-443, "7, 465-467 <DA2>
A;Cross-references: UNIPARC:UPI0000173650
R;Schmidt, J.J.; Sathyamoorthy, V.; DasGupta,
                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UP10000173652
A;Accession: S08573
A;Status: preliminary
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A;Residues: 2-17 <SCH2>
A;Cross-references: UNIPARC:UP10000173652
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169; Conserv
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Best Local S:
Matches 169
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tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani
N;Alternate names: tetanus neurotoxin
C;Space: Clostridium tetani
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
EMBO J. 5, Z495-2502, 1986
A;Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botu
A;Reference number: A25689; MUID:87053814; PMID:3536478
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A,Residues: 1-1315 <EIS>
A,Cross-references: UNIPARC:UPI000003617E; GB:X04436; NID:g40769; PIDN:C
A,Cross-references: UNIPARC:UPI000003617E; GB:X04436; NID:g40769; PIDN:C
R,Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A,Title: The complete nucleotide sequence of tetanus toxin.
A,Reference number: A25757; MUID:87040747; PMID:3774547
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A; Residues: 1-1315 < FAL>
A; Residues: 1-1315 < FAL>
A; Residues: 1-1315 < FAL>
A; Cross-references: UNIPARC: UP1000003617E; GB: X06214; NID: g40773; PIDN: CAA29564.1; PID: g
A; Cross-references: strain CN3911
B; Faliveather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
A; Faliveather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
A; Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in I
A; Reference number: A25194; MUID: 86085672; PMID: 3510187
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A;Molecule type: protein
A;Residues: 865-894 <FA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1082 RNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLVL-----VQYPD---R$KLYTG 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TQGGECSQNCVYALKLQSNLGNYGIGIFSIKNIVSKNKYCSQ 1219
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                                                                                                                                                                                                                                                                                                                                                121 WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYING 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 NLIDEKSISNLGDIHVSDNILFKI-VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 VEVIIR----KNGSTDISNTDNFVRK---NDLAYINVVDRDVEYRLYADISIAKPEKIIK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 LIRTSNSNNSLGQIIVMDSIGNNCTMNF----QNNNGGNIGLLGFHSNNLVASSWY---
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                                                                                                                                                                   SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                               88; Mismatches 156;
                            Score 580.5; DB 2
Pred. No. 8.4e-26;
                            25.4%;
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                                                                               Conservative
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A; Residues: 743-1315 <FA2>
                         Query Match
Best Local Similarity
Matches 140; Conserv
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C;Species: Clostridium botulinum
C;Saccession: S48106
R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
A;Reference number: S48103; MUD:94013372; PMID:8408542
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-367 < CAM>
A;Residues: 1-367 < CAM>
A;Residues: 1-367 < CAM>
A;Rose-references: UNIPROT:Q45861; UNIPARC:UPI00000B4F3D; EMBL:X70818; NID:g407784; PIC
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Superfamily: tetanus toxin
C;Reywords: neurotoxin
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A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Rossues: 1-1276 <BIN>
A;Crossuereferences: UNIPROT:P19321; UNIPARC:UPI0000126B83; EMBL:X54254; NID:g40395; PIDN
C;Superfamily: tetanus toxin
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R;Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, S.; Kriegls Nucleic Acids Res. 18, 5556, 1990
A;Title: Nucleotide sequence of the gene encoding Clostridium botulinum neurotoxin type A;Reference number: S11455; MUID:91016853; PMID:2216736
A;Accession: S11455
     EMBL Data Library, January 1993
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botulinum neurotoxin type D - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: L8-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                         214 SYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQF
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                                                                               Length 369;
                                                                                                                                    14; Indels
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                                                                                    DB 2;
A;Note: the nucleotide sequence was submitted to the C;Superfamily: tetanus toxin
                                                                               Query Match 28.2%; Score 645.5; DB 2
Best Local Similarity 77.9%; Pred. No. 3.4e-30;
Matches 120; Conservative 17; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                             WKISLNYNK---IIWTLQDTAGNNOKLVFNYTQM 151
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Best Local Similarity 71.8
Matches 107; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-84, 'P', 86-1291 <HAU>
A, Residues: 1-84, 'P', 86-1291 <HAU>
A, Cross-references: UNIPROT: Q93HT3; UNIPARC: UPI000016D75D; EMBL: X53751; NID: g14905; PIDMA, Cross-references: UNIPARCT: A murakami, T.; Indoh, T.; Yokosawa, N.; Takeshi, K.
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A;Title: The complete nucleotide sequence of the gene coding for botulinum type C-1 toxi A;Reference number: A35396; MUID:91024998; PMID:2222445
A;Accession: A35396
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A;Title: Cloning of the structural gene for Clostridium botulinum type C-1 toxin and who A;Reference number: A49777; MUID:91282468; PMID:2059039
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C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Baccession: S11291; A35396; S22166; A49777
R;Hauser, D; Eklund, M.W.; Kurazono, H.; Binz, T.; Niemann, H.; Gill, D.M.; Boquet, Nucleof Acids Res. 18, 4924, 1990
A;Title: Nucleotide sequence of Clostridium botulinum Cl neurotoxin.
A;Reference number: S11291; MUID:90370487; PMID:2204031
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SGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYI 178
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A; Residues: 1-669, R', 671-1291 <TS1>
A; Cross-references: UNIPARC:UP10000176709
R; Tsuruki, K', Kimura, K.; Fujii, N.; Yokosawa, N.; Oguma, K. R; Tsuruki, K.; Fujii, N.; Yokosawa, N.; Oguma, K. Rubmitted to the RMBL Data Library, December 1991
A; Description: Nucleotide sequence of the gene for one of the
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                                                                                                                                                          428
                                                                                                                                                                                                                  23.9%; Score 546; DB 2; L
31.5%; Pred. No. 8.2e-24;
live 82; Mismatches 169;
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A; Accession: $22166
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A,Molecule type: DNA
A,Residues: 1-1291 <TS2>
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Best Local Similarity
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A; Mesidues: 2-31 < LDEF>
A; Residues: 2-31 < LDEF>
A; Cross-references: UNIPARC: UPI000017364F
A; Cross-references: UNIPARC: UPI000017364F
C; Comment: The source of this protein was an extrachromosomal plasmid.
C; Comment: The precursor is cleaved by endogenous proteinase activity to form light (fradual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C; Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to ganglid C; Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. Function:
A. Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synaph
A. Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synaph
C. Superfamily: tetanus toxin
C. Superfamily: tetanus toxin
C. Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F. 2-457/Product: tentoxylysin light chain (fragment A) #status predicted <TTL>
F. 461-1315/Product: tentoxylysin heavy chain (fragment B.C) #status experimental <TTH>
F. 461-1315/Promain: channel forming (fragment B) #status predicted <TXC>
F. 865-1315/Domain: gangiloside binding (fragment C) #status predicted <TXC>
F. 233, 237/Binding site: zinc (His) #status predicted
F. 234/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation; epitope regions.

R; Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.

R; Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R.

R; Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolythe reference number: $27125; MUID: 93063293; PMID: 1331807

A; Reference number: $27125; MUID: 93063293; PMID: 1331807

R; de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.

Bur. J. Blochem. 229, 61-69, 1995

A; Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.

A; Reference number: $69348; MUID: 95262688; PMID: 7744050
                                                                                                                                                          the NH-2-terminal
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                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Readdues: 461-475 AMAT>
A; Readdues: 461-475 AMAT>
A; Cross-references: UNIPARC:UPI000017364E
R; Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, J. Immunol. 142, 394-402, 1989
A; Title: Delination of several DR-restricted tetanus toxin T cell epitopes.
A; Reference number: JS0098; MUID:89993918; PMID:2463305
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                                                                                                                                                          'n,
     A;Cross-references: UNIPARC:UPI000017364D
R;Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
Infect. Immun. 57, 3588-3593, 1989
A;Title: Isolation, purification, and characterization of fragment A;Reference number: A60759; MUID:90035436; PMID:2478476
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                                                                                                                                                                                                                                                                                                                                                                         Name=bont/f; Synonyms=bonT/F;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elmore M.J. Boddworth N.J., Whelan S.M., Minton N.P.;
Labore M.J., Boddworth N.J., Whelan S.M., Minton N.P.;
Labore M.J., Boddworth N.J., Whelan S.M., Minton N.P.;
Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.
R EMBL; L35496; AAA23210.1; -; Genomic_DNA.
R EMBL; L35496; Cintegral to membrane; IEA.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0006203; F:metallopeptidase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR001591; Botulinum.
R InterPro; IPR001595; Peptidase M27.
InterPro; IPR000525; Pept M Zn BS.
R Pfam; PF01742; Peptidase M27;
R PRINTS; RR00760; BONTOXILVSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=NCTC 10281;
Hutson R.A., Collins M.D.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
BONT/F (Neurotoxin type F)
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100.0%; Pred. No. 6.9e-128;
ive 0; Mismatches 0;
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Neurotoxin.
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Q9ZAJ9 CLOBO
P71117 CLOBO
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Q57236; Q45863;
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                                                                                                             (without alignments)
1375.940 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                     US-08-981-087B-1
2288
1 SYTNDKILLLYFNKLYKKIK.....TSSNGCFWSFISKEHGWQEN
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Q45861
Q84183
Q45849
Q91D87
P19321
                                                                                              2, 2006, 00:32:07 ; Search time 221 Seconds
              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    2166443 segs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BXG_CLOBO
Q45861_CLOBO
Q841S3_CLOBO
Q45849_CLOBO
Q91BS7_CLOBO
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778874 CLOBO
XA2 CLOBO
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092AJ8_CLOBO
093G71_CLOBO
BXB_CLOBO
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092AJ5_CLOBO
BAF_CLOBO
045851_9CLOT
09K395_CLOBU
054A79_CLOBU
09KZAJ3_CLOBU
09KZAJ3_CLOBU
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Maximum Match 100%
Listing first 45 summaries
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BXE CLOBU
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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1148 EGVEVIIRKNAPIDISNTDNFVRKNDLAYINVVDHGVEYRLYADISIIKSEKIIKLIRTS 1207
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              848 SYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQF 907
                                                                                                                                                                                                                                                                                                                                                                                                                                               358 NSNNSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGC 417
                                                                                  GIYSGRLSEVNIAQNNDIIYNSRYQNFSISFWVTIPKHYRPMNRNREYTIINCMGNNNSG
                                                                                                                                  121 WKISLNYNK---IIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIY
                                                                                                                                                                                                            178 INGNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDE
                                                                                                                                                                                                                                                                                          PDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLY
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MEDLINE=4401372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=TYPE F / ATCC 23387;
MEDLINE=199E F / ATCC 23387;
MEDLINE=29012902; PubMed=1398040; DOI=10.1016/0378-1097(92)90408-G;
East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A.,
Thompson D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             East A.K., Collins M.D., Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteolytic clostridium botulinum type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurocoxin type F precursor (EC 3.4.24.69) (BONT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence of the gene encoding type F neurotoxin of Clostridium bothlinum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulinum neurotoxin F heavy chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Type F / Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curr. Microbiol. 29:69-77(1994).
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1087
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                                                           NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                      1028 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP
                                                                                                                                        SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGV
                                                                                                                                                                                                                    EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                                                               1148 EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN
                                                                                                                                                                                                                                                                                              361 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CDC 3281;
MEDLINE=98440323; PubMed=9767710; DOI=10.1007/s002849900384;
MEDLINE=98440323; Collins M.D., East A.K.;
"Characterization of the genes encoding the Botulinum neurotoxin complex in a strain of clostridium botulinum producing type B & F neurotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium botulinum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.5%; Score 1887.5; DB 2; Length 1280; 82.4%; Pred. No. 5e-104; ive 32; Mismatches 41; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Santos-Buelga J.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y13631; CAA73972.1; -; Genomic_DNA.
RHSSP; Q45844; IBSH.
REROPS, MAT. 002; -.
GO; G0:0016021; C:integral to membrane; IEA.
GO; G0:0016021; F:metallopeptidase activity; IEA.
GO; GO:000465; P:pathogenesis; IEA.
GO; GO:000465; P:pathogenesis; IEA.
RO; GO:000465; P:pathogenesis; IEA.
InterPro; IPR011591; Botulinum.
R InterPro; IPR001395; Peptidase MAZ.
InterPro; IPR001395; Peptidase MAZ.
R PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PR00140; BONTOXILYSIN.
R PRODOM; PR00140; ZINC_PROTEASE; UNKNOWN I.
R PROSITE; PS00140; ZINC_PROTEASE; UNKNOWN I.
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Last annotation update)
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Q9ZAJS;
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Best Local Similarity 82.4*
Matches 357; Conservative
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NCBI_TaxID=1491;
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IDENTIFICATION OF SUBSTRATE

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WKISLNYNK---IIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIY 177
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                                                                                                                                       298 TGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKLIKLIRTS
                                INGNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDE
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EMBL; X68262; CAA48329.1; -; Genomic_DNA.

PIR; S33411; S33411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9325228; PubMed=8486245; DOI=10.1016/0378-1097(93)90581-L; Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D., Richardson P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium baratii.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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GO; GO:000827; F:metallopeptidase activity; IEA.
GO; GO:0008405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR000359; Peptidase_M27.
InterPro; IPR006035; Pept M Zn ES.
Pfam; PP01742; Peptidase_M27; I.
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Last annotation update)
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78.8%; Pred. No. 2e-100;
ive 38; Mismatches 5:
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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Q45851;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Best Local Similarity
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SEQUENCE
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8 5
                                                                                         botulinal neurotoxins and tetanus toxin.";

J. Biol. Chem. 269:1276-12772(1994).

J. Biol. Chem. 269:1276-12772(1994).

I. FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter release by internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 58-Gln-|-Lys-59 bond of synaptobrevins-1 and -2.

I. CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

I. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel community and community of community of the chain mediate channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              906
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                   Yamasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F., Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.; "Cleavage of members of the synaptobrevin/VAMP family by types D and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR012928; Toxin_recpt_bd_N.
InterPro; IPR012500; Toxin_trans.
Pfam; PP01742; Peptidase_MZ7; 1.
Pfam; PP07952; Toxin_trans; 1.
PRINTS; PR007960; BONTOXILYSIN.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulinum neurotoxin F light chain.
Botulinum neurotoxin F heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interchain (between light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: There are seven antigenically distinct forms botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
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Blasi J., Link E., Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chains) (Probable).
MW; 5B99756A7438B921 CRC64;
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EMBL; S73676; AAC60475.1; -; Genomic_DNA.
EMBL; X70820; CAA50151.1; -; Genomic_DNA.
EMBL; X70816; CAA50147.1; -; Genomic_DNA.
PIR; 140813; 140813.
PIR; S48109; S48109.
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Peptidase M27
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Matches 352; Conserv
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Length 1268;

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InterPro; IPR012500; Toxin
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SEQUENCE
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                                                                                                                                                          1LKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPNIFSNTRLYTGVE 301
                                                                                                                                                                                                             VIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNN 361
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A Wang X., Macgawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,
Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
T. "Genetic analysis of type E botulinum toxin-producing Clostridium
T. butyricum strains.";
Appl. Environ. Microbiol. 66:4992-4997 (2000).
EMBL; AB037714; BAB03522.; -; Genomic DNA.
REMBL; AB037716; BAB03521.; -; Genomic DNA.
REMBL; AB037710; BAB03521.; -; Genomic DNA.
REMBL; AB037710; BAB03520.; -; Genomic DNA.
REMBL; AB037710; BAB03520.; -; Genomic DNA.
REMBL; AB037711; BAB03520.; -; Genomic DNA.
REMBL; AB037711; BAB03521.; -; Genomic DNA.
REMBL; AB037701; BAB03511.; -; Genomic DNA.
REMBL; AB037707; BAB03515.1; -; Genomic DNA.
IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
                                                   KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN
                                                                                                      LIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPS
                                                                                                                                                                                                                                                                  SLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWSF
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR006025; Pept M. Zn. BS.
InterPro; IPR006035; PeptIdase_M27.
InterPro; IPR012928; Toxin_recpt_bd_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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MEDLINE=20509829; PubMed=11055954;
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Q9K395;
Q1-OCT-2000 (TrEMBLrel. 15, C:
01-OCT-2000 (TrEMBLrel. 15, Li
01-FEB-2005 (TrEMBLrel. 29, Li
Type E botulinum toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB037711; BAB03519.1;
EMBL; AB037709; BAB03517.1;
EMBL; AB037709; BAB03516.1;
EMBL; AB037707; BAB03515.1;
HSSP; Q45894; 1E1H.
SMR; Q9K395; 2-412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 SNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCF
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa Nakamura S., Karasawa T., Kozaki S., Seguence of the botulinum neurotoxin type E.", submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                   63.7%; Score 1458; DB 2; Length 1251; larity 62.7%; Pred. No. 1.9e-78; Conservative 75; Mismatches 74; Indels 12
                                                                                                                                UNKNOWN 1.
2021F4E427070296 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Botulinum neurotoxin type E.
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Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PR07923; Toxin, R. Dind, N; 1.
Pfam; PF07952; Toxin, trans; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; UN SEQUENCE 1251 AA; 143752 MW; 20
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|239 WNFISEEHGWQE 1250
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Q54A79;
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Matches 271; Conserv
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Best Local Similarity
Matches 276; Conserv
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949 GWKVSLANHELIWILGDNSGINQKLAFNYGNANGISDYINKWIFVIITNDRLGDSKLYIN 1008
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                                                                                                                                                                                                                                                                                                                    GVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKIIKLIR 355
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                                                                                                                                                                                                                                                       240 PSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS-NFLNINQQRGVYQKPNIFSNTRLYT 298
                                                                        61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNEYTIIDCIRNNNS
                                                                                                                            GWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYIN
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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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Wang X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y Yamakkawa K., Oguma K., Sakaguchi Y., Nakamura S.;
"Genetic analysis of type E botulinum toxin-producing Clostridium butyricum strains.";
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Clostridium.
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GG; GG: 000827; F:metallopeptidase activity; IEA.
GG; GG: 000827; F:metallopeptidase activity; IEA.
GG; GG: 000829465; P:pethogenesis; IEA.
GG; GG: 0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001591; Botulinum.
InterPro; IPR000395; Peptidase M27.
InterPro; IPR000395; Peptidase M27.
InterPro; IPR000355; Peptidase M27.
REANTS; PR00142; Peptidase M27; I.
REINTS; PR00142; Peptidase M27; I.
REINTS; PR001963; BONTOXILYSIN.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1255 AA; 143917 MW; 1B557B9DB5CDBEAD CRC64;
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Last sequence update)
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EMBL, AB039264; BAB12249.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
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MEDLINE=20509829; PubMed=11055954;
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                                      SYTDDKILLSYFWKFFKRIKSSSVLMMRYKNDKYVDTSGYDSNININGDVYKYPTWKNQF
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                     SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Trukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa Nakamoto K., Karasawa T., Kozaki S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB080207; BAC05434.1; -; Genomic_DNA.
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ProDom; PD001963; Botulinum; 1.
PROSTIE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1252 AA; 143510 MW; 41B633BB744D3B41 CRC64;
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GO:0008237; F:metallopeptidase activity; IEA.
GO:0009405; P:pathogenesis; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
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InterPro; IPR000625; Peptidase M27.
Pfam; PF01742; Peptidase M27; I.
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Matches 274; Conservative
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Q8KZM3;
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                                                      1 SYTNDKILILYPNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQP
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MEDLINE=90264400; PubMed=2160960;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
                          Gaps
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MEDLINE=92181428; PubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
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Q004962, Q45662,
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
(Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain;
                          17;
                          71; Indels
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         Pred. No. 1.6e-77;
                          Mismatches
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63.0%; F1.
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                                                                                                                                                                                                                                                                                                               Gimenez J.A., Dasgupta B.R.; "Botulinum neurotoxin type B fragmented with endoproteinase Lys-C "Botulinum neurotoxin type B fragmented with tetanus neurotoxin."; Biochimie 72:213-217(1990).
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MEDIINE=94013372; PubMed=8408542;

Campbell K.D., Collins M.D., Bast A.K.;

"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";

J. Clin. Microbiol. 31:2255-2262(1993).
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long as its content is in no way modified and this statement
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                                                                                                                                                                                                                                                                                  MEDLINE=90344918; PubMed=2116911; DOI=10.1016/0300-9084(90)90075-R
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                                                  PROTEIN SEQUENCE OF 1-13.
MEDLINE=85197963, Pubmed=9888113;
MEDLINE=8197963, Pubmed=9888113;
MEDLINGE JJ., Sathyamoorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neux
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EMBL; X62683; CAA44558.1; -; Genomic_DNA.
EMBL; X70815; CAA50146.1; -; Genomic_DNA.
Chem. 265:9153-9158(1990)
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PIR; S21178; S21178.

PDB; 1T3A; X-ray; A/B=1-421.

MEROPS; M27.002; --
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  Biol.
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STRAIN=BL6340
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                                                                                                                                                                                                                                                                                                                                                                                                                                     887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPD 239
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                            Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heavy chains) (Probable).

R -> G (in Ref. 2).
C -> S (in Ref. 2).
R -> A (in Ref. 2 and 3).
FE -> L (in Ref. 2 and 6).
FE -> LQ (in Ref. 2 and 6).
N -> NN (in Ref. 2 and 6).
                                                                     Pfam; PF07952; Toxin_trans; 1.

PRINTS; PR00760; BONTOXILYSIN.

Probom; P001965; Botulinum; 1.

PROSITE; P001965; ZINC_PROTEASE; 1.

3D.structure; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
                                                                                                                                                         Botulinum neurotoxin E light chain.
Botulinum neurotoxin E heavy chain.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                           ; Score 1429; DB 1; Length 1250; ; Pred. No. 1e-76; 73; Mismatches 72; Indels 18;
                                                                                                                                                                                                                                                                                                                                     D9FCE26DDA041EB4 CRC64;
                    InterPro; IPR012928; Toxin_recpt_bd interPro; IPR012500; Toxin_trans Pfan; PF01742; Peptidase M27; 1. Pfan; PF07953; Toxin_R bind N; 1. Pfan; PF07952; Toxin_trans; 1.
Pept M Zn BS.
Peptidase M27
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Best Local Similarity 62.5
Matches 272; Conservative
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Created) Last sequence update) Last annotation update)

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BXE. CLOBU P30995; 01-JUL-1993 01-JUL-1993 13-SEP-2005

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STANDARD;

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its usé as long as its content is in no way modified and this statement is not
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Giments J., Foley J., Dasgupta B.R.;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";
PASEB J. 2.41750-41750(1988)
-:- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter
release. It binds to peripheral neuronal synapses, is internalized
and moves by retrograde transport up the axon into the spinal cord
where it can move between postsynaptic and presynaptic neurons. It
inhibits neurotransmitter release by acting as a zinc
                                                                                                                                                                                                                                                                                                          MEDLINE-91237316; PubMed-2033376; Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.; Tramana K.; Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340."; J. Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                      Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
                                               Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E) (Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain;
                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 183:107-113(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X62088; CAA43998.1; -; Genomic_DNA.
EMBL, X53180; CAA37321.1; -; Genomic_DNA.
PIR; JH0256; JH0256.
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InterPro; IPR000395; Peptidase_M27.
InterPro; IPR012928; Toxin_recpt_bd_N.
InterPro; IPR012500; Toxin_trans.
Pfam, PF01742; Peptidase_M27; 1.
Pfam, PF07953; Toxin_R_bind_N, 1.
Pfam, PF07955; Toxin_trans; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Botulinum; 1.
                  (Bontoxilysin E) [Contains: Botulinu
Botulinum neurotoxin E heavy chain].
                                                                                                                                                STRAIN=ATCC 43181, and ATCC 43755;
MEDLINE=92181428; PubMed=1543481;
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                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 1-251.
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                                                                                                                                  NUCLEOTIDE SEQUENCE.
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SMR; P30995; 1-411.
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                                                                                 Clostridium.
NCBI_TaxID=1492;
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948 GWKVSLNHNEIIWTLODNSGINOKLAFNYGNANGISDYINKWIFVTIINDRLGDSKLYIN 1007
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MEDLINE=90235864; PubMed=2185020;
MEDLINE=90235864; PubMed=2185020;
Thompson D.E., Brehm J.K., Oultram J.D., Swinfield T.-J., Shone C.C.,
Atkinson T., Melling J., Minton N.P.;
"The complete amino acid sequence of the Clostridium botulinum type A
GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLNNBYTIIDCIRNNNS
                                                                                                                                                                                     1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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                                                                                                                                                                   Gaps
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01-JUL-1989 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-
                                                        Botulinum neurotoxin E light chain.
Botulinum neurotoxin E heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                    18;
                                                                                                                                                 ; Score 1426; DB 1; Length 1250; Pred. No. 1.5e-76; 73; Mismatches 71; Indels 18.
                                                                                                                               MW; 8171B5B2C2312857 CRC64;
                                                                                                               chains) (Probable)
K -> M (in Ref. 2)
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1235 GFFWNFISEEHGWQE 1249
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P10845; P01561; P18639;
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                                                                                                                                                          Similarity
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Dasgupta B.R., Foley J., Niece R.; "Partial sequence of the light chain of botulinum neurotoxin type A."; Biochemistry 26:4162-4162(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Type A / NIH;
MEDLINE=96096783; PubMed=8521962; DOI=10.1016/0014-5793(9S)01241-5;
Fujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K.;
"Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins.";
FEBS Lett. 376:41-44(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97016817; PubMed=8863443;

MEDLINE=97016817; PubMed=8863443;

Bast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteclytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";

Int. J. Syst. Bacteriol. 46:1105-1112(1996).
                                                                                                                                                                                                                                                                               Binz I., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.; "The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins"; J. Biol. Chem. 265:9153-9158(1990).
neurotoxin, deduced by nucleotide sequence analysis of the encoding
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MEDLINE=91120847; PubMed=2126206; DOI=10.1016/0300-9084(90)90048-L;
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MEDLINE=89024662; PubMed=3178218;
Sathymocorthy V., Dasgupta B.R., Foley J., Niece R.L.;
"Botulinum neurcoxin type A: cleavage of the heavy chain into two halves and their partial sequences.";
Arch. Biochem. Biophys. 266:142-151(1988).
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Schmidt J.J., Sartymoorthy V., Dasgupta B.R.;
"Partial amino acid sequence of the heavy and light chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dasgupta B.R., Dekleva M.L., "Botulinum neurotoxin type A: sequence of amino acids at the terminus and around the nicking site.";
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[11]
PROTEIN SEQUENCE OF 866-879 AND 1147-1218.
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MEDLINE=90264400; PubMed=2160960;
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MEDLINE=89350959; PubMed=2669749;
                                                                             Sur. J. Biochem. 189:73-81(1990)
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1034 LIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNS 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IPR011591; Botulinum.
R InterPro; IPR011591; Pept M Zn BS.
R InterPro; IPR001295; Peptidase M27.
R InterPro; IPR012929; Toxin_recpt_bd_N.
R InterPro; IPR012929; Toxin_recpt_bd_N.
R Pfam; PR01742; Peptidase M27; 1.
R Pfam; PR01742; Peptidase M27; 1.
R Pfam; PR07952; Toxin_trans; 1.
R PRINTS; PR00760; BONTOXILYSIN.
R PRODO; PB001955; BCULinum; 1.
R PROSTIE; PS00142; ZINC_PROTEASE; 1.
R PROSTIE; PS00142; ZINC_PROTEASE; 1.
R MOSTIE; PS00142; ZINC_PROTEASE; 1.
R MACATILIOPROCEASE; Neurotoxin; Pharmaceutical; Protease; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E->A: Drastic decrease in enzymatic
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Botulinum neurotoxin A heavy-chain.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interchain (between light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1120.5; DB 1; Length 1295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.6e-58;
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Zinc (catalytic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (catalytic)
X92973; CAA63551.1; -; Genomic_DNA.
D67030; BAA11051.1; -; Genomic_DNA.
M27892; AAA23269.1; -; Genomic_DNA.
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                                                                                                   PDB; 3BTA; X-ray; A=1-1295
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                                                                            PIR; A35294; BTCLAB
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                                                                                                                          MEROPS; M27.002;
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INIT MET
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Best Local Simi
Matches 219;
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TRANSMEM
ACT SITE
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DISULFID
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy chain (H).

-!- SUBCELDILAR LOCATION: Secreted.
-!- FARMACEUTICAL: Available under the name BOTOX (Allergan) for the reatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.
-!- MISCELLANBOUS: There are seven antigenically distinct forms of both in meurotoxin: Types A, B, Cl. D, E, P, and G.
-!- SIMILARITY: Belongs to the peptidase M77 family.
-!- DATABASE: NAME=BOTOX product information Web site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lorrange 19. 5.898-902(1998).

-I- FUNCTION: Inhibite acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gin-1-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
MEDLINES-98455071; PubMed=9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
COFACTOR: Binds 1 zinc ion per subunit.
SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WWW="http://www.botox.com/site/".
DATABASE: NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;
WWW="http://www.expasy.org/spotlight/back_issues/sptlt019.shtml".
                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION OF SUBSTRATE.
MEDLINE=94124495; PubMed=8294407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C., Jahn R., Niemann H.;
"Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
J. Biol. Chem. 269:1617-1620(1994).
                                                        72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                  "Botulinum neurotoxins serctypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds.";
FEBS Lett, 335:99-103(1993).
                                                                                                                                                                        MEDLINE=94063091; PubMed=8443676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati P., Wilson M.C., Montecucco C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
"Site-directed mutagenesis identifies active-site residues of the light chain of botulinum neurotoxin type a.';
Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
                                                          97,
          PubMed=8397793;
Gimenez J.A., DasGupta B.R.;
"Botulinum type A neurotoxin digested with pepsin yields 132,
45, 42, and 18 kD fragments.";
J. Protein Chem. 12:351-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of
the European Bioinformatics Inst
                                                                                                                                                           DENTIFICATION OF SUBSTRATE
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240

12 RESULT

EMBL; X52066; CAA36289.1; -; Genomic\_DNA. EMBL; M30196; AAA23262.1; -; Genomic\_DNA.

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Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 LIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
                                                                                                                                                                                                                                                                                                                                                          STRAIN=Allergan-Hall A;
MEDLINE=22919384; PubMed=14557061; DOI=10.1016/S0378-1119(03)00792-3;
Zhang L., Lin W.J., Li S., Aoki K.R.;
"Complete DNA sequences of the botulinum neurotoxin complex of
Clostridium botulinum type A-Hall (Allergan) strain.";
Gene 315:21-32(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                       Dineen S.S., Bradshaw M., Johnson E.A.;
"Neurotoxin gene clusters in Clostridium botulinum type A strains:
sequence comparison and evolutionary implications.";
Curr. Microbiol. 46:845-352(2003).
                                                                                                                                                                                                                       STRAIN=Hall A-hyper;
MEDLINE=22617869; PubMed=12732962; DOI=10.1007/800284-002-3851-1;
                                                                                                                                   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.4%; Pred. No. 2.0e-50,
tive 78; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1296 AA; 149425 MW; DEA8CF2754AE43E6 CRC64;
                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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 PRT; 1296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF461540; AAM75961.1; -; Genomic DNA
EMBL, AF488749; AAQ06331.1; -; Genomic_DNA
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                              10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                 10-MAY-2005 (TrEMBLrel. 30 BONT/A (Neurotoxin BONT).
Q7B8V4_CLOBO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 219; Conservative
                                                                                                     Name=bont/a;
Clostridium botulinum.
                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                        NCBI_TaxID=1491;
                                                                                                                                                        Clostridium.
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PRT; 1295 AA.

STANDARD;

RESULT 13 BXA2\_CLOBO ID BXA2\_CLOBO

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                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=TYPe A / Kyoto-F;
MEDLINE=94143603; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Willems A., East A.K., Lawson P.A., Collins M.D.,
"Sequence of the gene coding for the neurotoxin of Clostridium
botulinum type A associated with infant botulism: comparison with
other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
                                                    28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (BC 3.4.24.69) (BONT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-
                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                  chain; Botulinum neurotoxin A heavy-chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; I40645; I40645.
PDB; 1E1H; X-ray; A/C=9-249, B/D=250-415.
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EMBL; X87974; CAA61234.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011591; Botulinum.
InterPro; IPR0105025; Pept M Zn BS.
InterPro; IPR010395; Peptidase-M27.
InterPro; IPR010398; Poxin recpt bd.N.
InterPro; IPR012500; Toxin recpt bd.N.
InterPro; IPR012500; Toxin recpt bd.N.
Pfam; PF01953; Toxin R bind.N; 1.
Pfam; PF07953; Toxin Lrans; 1.
PRINTS; PR07760; BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Type A / Kyoto-F;
MEDLINE=97016817; PubMed=8863443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD001963; Botulinum; 1
                                                                                                                                                                                               Name=botA; Synonyms=atx, bna;
Clostridium botulinum.
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Clostridium botulinum
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PS00142; ZINC_PROTEASE; FALSE_NEG.
.ure; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin;
                                Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
                                                                                                                                                                                                                                                                                              47.7%; Score 1092.5; DB 1; Length 1295; 48.6%; Pred. No. 1.2e-56;
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                                                                                                                                                                                                                                                                                                              48.6%; Pred. No. 1.26-20,
tive 76; Mismatches 133; Indels
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AA; 149280 MW; 5DA04A13D98D6372 CRC64;
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Clostridium botulinum.
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ID Q58GH1;
AC Q58GH1;
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"Gene probes for identification of the botulinal neurotoxin gene and
specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                          19; Gaps
WICLEOTIDE SEQUENCE.
SMITAIN-FRI-HIAD.
Smith T.J., Lou J., Geren I., Forsyth C., Tsai R., Tepp W.H.,
Bradshaw M., Johnson E.A., Smith L.A., Marks J.D.;
Bradshaw M., Johnson E.A., Smith L.A., Marks J.D.;
Sequence variation within botulinum neurotoxin serotypes impacts
antibody binding and neutralization.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
BRBL; APS3275; AAX53156.1; -; Genomic_DNA.
Neurotoxin.
SEQUENCE 1296 AA, 149410 MW, 6F12E7BF28ED69DI CRC64;
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                                                                                                                                                                                                                                                                                   47.7%; Score 1092.5; DB 2; Length 1296;
48.6%; Pred. No. 1.2e-56;
Live 76; Mismatches 133; Indels 19;
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MEDLINE=94013372; PubMed=8408542;
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                                                                                                                                                                                                                                                                                                                    Best Local Similarity 48.6%
Matches 216; Conservative
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RA Campbell K.D.;

RE Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.

BE EMBL; X70821; CAA50152.1; -; Genomic_DNA.

DR HSRP; P04958; JA8D.

DR GO; GO:0009405; P:pathogenesis; IEA.

KW Neurotoxin.

FT NON_TER 366 366

SQ SEQUENCE 366 AA; 43136 MW; 45A132B235D7E640 CRC64;

Cuery Match 35.7%; Score 816; DB 2; Length 366;

Best Local Similarity 100.0%; Pred. NO: 8.3e-41;

Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A SYTUDKILILYPHYLYKKINDSILDMRYENNKFIDISGYGSNISINGDVYIYSTURNOF 07

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CA STUDKILILYPHYLYKINGNOBILDMRYENNKFIDISGYGSNISINGDVYIYSTURNOF 07

CA STUDKILILYPHYLYKINGNOBILDMRYENNKFIPKYFNKVNIANNEYTIIDCIRNNNSG 120

CA STUDKILILYPHYLYMRYIMTLQDTAGNNOKLVFNYTQMIS 153

CA STUDKILILYPHYLIMTLQDTAGNNOKLVFNYTQMIS 153

CA STUDKILILYPHYLIMTLQDTAGNNOKLVFNYTQMIS 366

DD 334 WKISLNYNKIIWTLQDTAGNNOKLVFNYTQMIS 366
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Search completed: March 2, 2006, 00:46:23 Job time : 224 secs

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US-08-913-880C-11
US-08-913-880C-10
US-08-913-880C-1
US-08-110-786A-8
US-09-465-276-1
US-09-467-114A-22
US-09-417-485D-6
US-09-114-085D-6
US-09-114-001C-2993
US-08-480-604A-6
US-08-915-136-6
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## ALIGNMENTS

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

572060 seqs, 82675679 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

RESULT 1 115-08-488-604A-28	; Sequence 28, Application US/08480604A ; Patent No. 5736139 ; GENERAL INFORMATION.	5523	ADDRESSEE: MEDLEN & CARROLL, LLP STREET: 220 MONTCOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFOONIA	COUNTRY: UNITED STATES OF AMERICA	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IRM PC COMDETIBLE	OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version #1.30	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/480,604A	; FILING DATE: 07-JUN-1995 ; CLASSIFICATION: 424	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/422,711	; FILING DATE: 14-APR-1995 ; PRIOR APPLICATION DATA:	; APPLICATION NUMBER: US 08/405,496 ; FILING DATE: 16-MAR-1995	PRIOR PARTICULATION DATA:	FILING DATE: 25-OCT-1994	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/161,907	; FILING DATE: 02-DEC-1993	APPLICATION NUMBER: US 07/985,321	ON DATA	; APPLICATION NUMBER: US 07/429,791 ; FILING DATE: 31-OCT-1989	; ATTORNEY/AGENT INFORMATION:	REGISTRATION NUMBER: 40,027	
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		* * : dad. dad.: :	l by chance to have a the result being printed, ce distribution.		Description	Sequence 28, Appl Sequence 28, Appl	28,	23,	Sequence 23, Appl	26,	26,	219,	Sequence 9, Appli Sequence 9, Appli	Sequence 220, App Sequence 20, Appl	C) C	34.	4 'C	Sequence 17, Appl Sequence 16, Appl	15,	Sequence 14, Appl Sequence 13, Appl	
2000000000	n Match 0% n Match 100% } first 45 summaries	<pre>vued_Patents AA:* /cgn2_6/ptodata/1/iaa/5_COMB.pep:* /cgn2_6/ptodata/1/iaa/6_COMB.pep:* /cgn2_6/ptodata/1/iaa/H_COMB.pep:* /cgn2_6/ptodata/1/iaa/RE_COMB.pep:* /cgn2_6/ptodata/1/iaa/RE_COMB.pep:* /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*</pre>	. No. is the number of results predicted by chance to he greater than or equal to the score of the result being derived by analysis of the total score distribution.	SUMMARIES	ength DB ID	1296. 1 US-08-480-604A-28	2 2 2	Sin Sin	77	٠.		7 (7)	0 0				H H	01 01	100		
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
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                                                                                                                                                                                                                                                                                                                                                                                                62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
                                                                                                                                                                                                                                                                                                                    2 YTNDKILLILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.4%; Pred. No. 9.7e-83;
Matches 219; Conservative 78; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
    OPHD-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1271 IERSSRTLGCSWEFIPVDDGWGE 1293
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US-08-405-496A-28
; Sequence 28, Application US/08405496A
; Patent No. 5919665
REFERENCE/DOCKET NUMBER: OPH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                             TYPE: amino acid
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49.4%; Pred. No. 9.7e-83;
:ive 78; Mismatches 127;
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154

FILING DATE: 25-OCT-1994

PRIOR APPLICATION NUMBER: US 08/161,907

FILING DATE: 02-DEC-1993

PRIOR APPLICATION NUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

PRIOR APPLICATION NUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

PRIOR APPLICATION NUMBER: US 07/429,791

FILING DATE: 31-OCT-1989

ATTORNEY/AGENT: NUMBER: 40,027

REFERENCE/DOCKET NUMBER: QPHD-01308

TELEPONMUNICATION INFORMATION:
TELEPANG: (415) 397-8338

INPORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:

LUMPORMATION FOR SEQ ID NO: 28:
CHARACTERISTICS:
CHARACTERIS
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GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.4%;
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
    241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQORGVYQKPNIFSNTRL 296
                                                                                           297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: HAVENSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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PRICATION NUMBER: US 08/329,154
PRICATION DATE: 25-0CT-1994
PRICATION DATA:
APPLICATION NUMBER: US 08/161,907
PRICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
PRICATION NUMBER: US 07/985,321
PRICATION NUMBER: US 07/995,321
PRICATION NUMBER: US 07/995,321
PRICATION NUMBER: US 07/99791
PRILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                     408 IRKNISSNGCFWSFISKEHGWQE 430
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APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palace
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; Sequence 28, Application US/09084517
; Patent No. 6613329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
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APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1296;
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE CORRESPONDED ADDRESSE: 32 CORRESPONDED & CARROLL, LLP STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 49.0%; Score 1120.5; DB 2; Length Best Local Similarity 49.4%; Pred. No. 9.7e-83; Matches 219; Conservative 78; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
UNRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELLICATION DATA:

APPLICATION NUMBER: US 08/405,496
PILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1989
ATTICKNEY/AGENT INFORMATION:
NAME: INGOLAR DEC-1992
PRIOR DATE: 31-OCT-1989
ATTICKNEY/AGENT INFORMATION:
NAME: INGOLAR DATAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPHD-01763
                                                                                                                                                                                                               UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPI
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TELEPHONE: (415) 705-8410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1296 amino acids
amino acid
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                                                                                                                                                                                         CALIFORNIA
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                                                                                                                                                                                                                                 ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155 YRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVVKKKEYRLATNASQAGVEKILSALEI 1211
                                                                                                                                                                                                                                         LENLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSCW 974
                                                                                                                                                                                                                   122 KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN 181
                                                                                                                                                                                                                                                                                         LIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDP 240
                                                                                                                                                                                                                                                                                                                                                              SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                  297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
                                                                                                                                            62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
                                                                          2 YTUDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
                                      19;
 Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: STARPORD, DOUGLAS C.
APPLICANT: STARPORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
 49.0%; Score 1120.5; DB 2; Length
49.4%; Pred. No. 9.7e-83;
ive 78; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US/08/480,504A
FILING DATE: 14-APR-1995
PRIOR APPLICATION NUMBER: US 08/402,711
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1271 İERSSRTLĞCSWEFİPVDDĞWGE 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALIFORNIA
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94104
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US-08-480-604A-23
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123 GEIIWTLODTOBIKORVVFKYSOMINISDYINRWIFVTITNNRLNNSKIYINGRLIDOKP 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 WGNYLLYNKRYYLLNLLRIDKSITQNS----NFLNINQORGVYQKPNIFSNTRLYTGVEV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 IIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 LGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNNIRKNTS 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 ISNLGNIHASNNIMPKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLES
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Retent No. 5919665
GENERAL NO. FORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: NACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NETROTOXIN
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 48.7%; Score 1113.5; DB 1; Best Local Similarity 49.9%; Pred. No. 8.5e-83; Matches 218; Conservative 75; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                       NAME: INGOLIA, DIANE E.
REGISTRATION VIMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELEPANTUNICATION INFORMATION:
TELEPANE: (415) 705-8410
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                              PELLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
FILING DATE: 25-OCT-1994
FILING APPLICATION DATA:
ADDITORMEN: 25-OCT-1994
ADDITORMEN: 25-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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127 122

67 63

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359 LSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSR 418
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PROBLY, OSBER N.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT TITLE OF INVENTION: PERVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS S.
ADDRESSEE: ADDRESS S.
CORRESPONDENCE ADDRESS S.
ADDRESSEE: ADDRESS S.
ADDRESSEE: ADDRESS S.
CONTEST: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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48.7%; Score 1113.5; DB 2;
Best Local Similarity 49.9%; Pred. No. 8.5e-83;
Matches 218; Conservative 75; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
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PRIOR DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
PILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
PILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
PILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIAME E:
NAME: INGOLIA, DIAME E:
NAME: INGOLIA, DIAME E:
NAME: INGOLIA, DIAME E:
NAME: OF TABLES O
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08915136 Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/480,604
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                414 SNGCFWSFISKEHGWQE 430
                                                                                                                                                                                   419 TLGCSWEFIPVDDGWGE 435
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 438 amino acids
amino acid
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APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-915-136-23
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
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                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
                                                                                                     : 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
PRILING DATE: 25-0CT-1994
PRILING DATE: 25-0CT-1994
PRILING DATE: 02-DEC-1993
FRILING DATE: 02-DEC-1993
PRILING DATE: 02-DEC-1993
PRILING DATE: 04-DEC-1992
PRILING DATE: 04-DEC-1992
PRILING DATE: 01-0CT-1989
APPLICATION NUMBER: US 07/429,791
APPLICATION NUMBER: US 07/429,791
REGISTRATION NUMBER: US 07/429,791
REGISTRATION NUMBER: OPHD-01308
TELECOMMUNICATION INPRORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: OPHD-01308
TELECOMMUNICATION INPORMATION:
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TELECOM
                                                                CARROLL, LLP
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 amino acids
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MOLECULE TYPE: protein
                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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STATE: CA
COUNTRY:
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243 WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKF 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADRESS: ADDRESSE: ADDRESSE: CARROLL, LLP STREET: 220 MONTGOMERY STREET, SUITE 2200
SITY: SAN FRANCISCO STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                                                                                                                  48.7%; Score 1113.5; DB 2; 49.9%; Pred. No. 8.5e-83; ive 75; Mismatches 125;
FILING DATE: 31-OCT-1989
ATTORNEY/AGBNT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REPERBROKE/DOCKET NUMBER: 0PHD-01610
TELECHONE: (415) 705-8410
TELEPAN: (415) 705-8410
TELEPAN: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08480604A; Patent No. 5736139; GENERAL INFORMATION:
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Matches 218; Conservative
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                     amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 ISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDF 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGQIIVMDS-----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNNIRKNTS 413
                                                                                              SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127
                                                                                                                                                                                          NKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKS 187
                                                                                                                                                                                                                                                                                                                                                                                  247 WGNYLLYNKRYYLLNLLRIDKSITQNS----NFLNINQQRGVYQKPNIFSNTRLYTGVEV 302
  LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
                             TREATMENT AND DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/084,517 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERGTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-WAR-1995
FRICH APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 23, Application US/09084517; Patent No. 6613329; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 SNGCFWSFISKEHGWQE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 TLGCSWEFIPVDDGWGE 435
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US-09-084-517-23
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128 NKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKS 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.7%; Score 1113.5; DB 1; Length 462; 49.9%; Pred. No. 9.2e-83; Live 75; Mismatches 125; Indels 19;
                                                                                                                                                         Sequence 26, Application US/08405496A
Patent No. 5919665
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/405,496A FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTCOMENY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154

FILING DATE: 25-CCT-1994

PRIOR APPLICATION NUMBER: US 08/161,907

PILING DATE: 02-DEC-1993

PRIOR APPLICATION NUMBER: US 07/985,321

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION UNMER: US 07/995,791

FILING DATE: 31-CCT-1989

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPHD-01308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: INCOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                    414 SNGCFWSFISKEHGWOE 430
                                          : || | | : || |
443 TLGCSWEFIPVDDGWGE 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
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Best Local Similarity 49.9
Matches 218; Conservative
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                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3(
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
                                                                                                                                                                                                                                                                                                                                          PELICATION NUMBER: US 08/329,154
PILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       PRIOR APPLICATION 1213.

PRIOR APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-NAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET UNMBER: 0PHD-01763
TELECOMMUNICATION:
TELEPHONE: (415) 705-8410
                                                                                                              UMBER: US/08/480,604A
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ 1D NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 462 amino
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amino acid
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US-08-480-604A-26
                                                                                                                                                     FILING DATE: 0 CLASSIFICATION:
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267 WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKF 326
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                                                                                                                                                                                                                                                                                                                                                                                                                    88 SKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNY
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                                                                                                                                                                                                                      DB 2; Length 462;
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APPLICANT: KINK, JOHN A.
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                    48.7%; Score 1113.5; DB 2; Length
49.9%; Pred. No. 9.2e-83;
tive 75; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
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; Sequence 26, Application US/09084517
; Patent No. 6613329
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 SNGCFWSFISKEHGWQE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 TLĠĊSWEFIPVDDĠWGE 459
                                                                                                                                                                                                                                                                Matches 218; Conservative
                                                                                                                                                   , MOLECULE TYPE: protein US-08-915-136-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                   207 ISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDF 266
                                                                                                                      267 WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKF 326
                                                                                                                                                                                IIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNS 362
                                                                                                                                                                                                        WGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRLYTGVEV 302
                                                                                                                                                                                                                                                                     LGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNNIRKNTS 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PIRCA, JOSEPH R.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: MEDLEN & CARROLL, LLP
220 MONTGOMERY STREET, SUITE 2200
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
FILING DATE: 16-MAR-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1997
FILING DATE: 04-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/429,791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/08915136
Patent No. 6290960
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
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FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94104
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STREET: 22
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APPLICANT: Leenhouts, Cornelis J.

APPLICANT: Leenhouts, Cornelis J.

TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way FILE REPERENCE: 2183-5673

CURRENT APPLICATION NUMBER: US/10/360,101

CURRENT RILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 309

SOFTWARE: PatentIn version 3.1

SEQ ID NO 219

LENGTH: 848
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: sequence A-heavy chain of clostridium botulinum toxin type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 SNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SILKDFWGNYLLYNKRYYLLNILRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 KISLAYAKIIWTLODTAGNAQKLVFNYTQMISISDYINKWIFVTITANRLGNSRIYINGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
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                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 19;
                                                                                                                                                                                                                                                                                                                                                                       Length 848;
                                                                                                                                                                                                                                                                                                                                                                     47.7%; Score 1092.5; DB 2;
48.6%; Pred. No. 1.1e-80;
tive 76; Mismatches 133; 1
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APPLICANT: Steward, Lance E.
APPLICANT: Sachs, George
APPLICANT: Sachs, George
TITLE OF INVENTION: Methods and Compositions for tritle OF INVENTION: Methods and Compositions for tritle OF INVENTION: Treatment of Pancreatitis
FILE BEFERENCE: 17282
CURRENT APPLICATION NUMBER: US/09/288,326A
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ. ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6776990
                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 48.6*
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                     US-10-360-101-219
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LENGTH: 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRLYTGVEV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 WGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKF 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGQIIVMDS-----IGNNCTMNFQNNNGGNIGLLGFHSNN----LVASSWYYNNIRKNTS 413
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49.9%; Pred. No. 9.2e-83;
iive 75; Mismatches 125
                                                                                                                                                                                     FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTONNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: 32,837
        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 25-OCT-1994
                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 219, Application US/10360101 Patent No. 6861236 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 218; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
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                                                                                                                                                                                                                                                                   INTESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW
                                                                                                                                                                                                                           62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
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                                                                                                  Length 382;
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; Pred. No. 3.4e-75;
65; Mismatches 102; Indels
                                                                                           Query Match

44.6%; Score 1019.5; DB 2; Length
Best Local Similarity 51.4%; Pred. No. 3.4e-75;
Matches 197; Conservative 65; Mismatches 102; Indels
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APPLICANT: Aoki, K. Roger
APPLICANT: Sacia, George
APPLICANT: Sacia, George
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treament of Pancreatitis
FILE REPRENCE: 17282CIF(AP)
CURRENT FILING DATE: 2000-04-13
FRIOR PELICATION NUMBER: US 09/288,326
FRIOR PILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 12
SOPTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Clostridium botulinum
ORGANISM: Clostridium Botilinum
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Best Local Similarity 51.4%;
Matches 197; Conservative 6
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US-09-548-409B-9
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1050.055 Million cell updates/sec
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2288
1 SYTNDKILLIYPNKLYKKIK.....TSSNGCFWSFISKEHGWQEN
                                                                  March 2, 2006, 01:11:03 ; Search time 171.5 Seconds
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.: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.ppp: *
.: /cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp: *
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-452-024-152
US-10-205-516-12
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US-10-478-516-7
US-10-130-973A-7
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US-10-130-973A-14
                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                           1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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Match
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1000.0
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Maximum DB &
                                              OM protein
                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                                                                                                          Database
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28 1833 80.1 1274 5 US-10-728-696-71 Sequence 71, Appl 29 1833 80.1 1274 6 US-11-001-241-71 Sequence 71, Appl 30 1827 79.9 1268 4 US-10-01-241-56 Sequence 71, Appl 31 1800 78.7 448 4 US-10-254-774-73 Sequence 73, Appl 32 1800 78.7 448 4 US-10-271-012-73 Sequence 73, Appl 34 1800 78.7 448 5 US-10-271-012-73 Sequence 73, Appl 35 1800 78.7 448 5 US-10-29-032-73 Sequence 73, Appl 36 1800 78.7 448 5 US-10-729-527-73 Sequence 73, Appl 37 1800 78.7 448 5 US-10-279-888-73 Sequence 73, Appl 39 1458 63.7 448 6 US-10-278-898-73 Sequence 73, Appl 40 1457.5 63.7 452 4 US-10-1641-73 Sequence 73, Appl 40 1457.5 63.7 452 4 US-10-1641-14 Sequence 56, Appl 41 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 44 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 44 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 44 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 45 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 45 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 46 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 47 1457.5 63.7 452 4 US-10-21-56 Sequence 56, Appl 47 1457.5 63.7 452 4 US-10-22-56 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56, Appl 56 US-10-729-556 Sequence 56,
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### ALIGNMENTS

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US-08-981-087A-1
Sequence 1, Application US/08981087A
Sequence 1, Application US/08981087A
Publication No. US20020081304A1
GENERAL INFORMATION:
APPLICANT: Elmore, Michael J.
APPLICANT: Elmore, Michael J.
APPLICANT: Paeschnik, Vladimir A.
APPLICANT: Paeschnik, Vladimir A.
APPLICANT: Paeschnik, Vladimir A.
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APPLICANT: Paeschnik, Vladimir A.
APPLICANT: Paeschnik, Vladimir A.
APPLICANT: Vladimir A.
APPLICANT: Vladimir A.
CORRESPONDENCES: ADROPESS:
ACORNITS: USA
CONNTRS: USA
CONNTRS: USA
CONNTRS: Tall MP C Compacible
COMPUTER READABLE CORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE CORM
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1995
APPLICATION NUMBER: 25,327
REFERENCE/POCKET NUMBER: 25,327
REFERENCE/POCKET NUMBER: 124-688
TELECOMMUTION NUMBER: 123-16400
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEMOTH: 431 amino acids
TTYPE: Amino acids
TTYPE: Amino acids
TTYPE: Amino acids
TTYPE: Amino acids
TTYPE: Amino acids
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            Length 431;
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GENERAL INFORMATION:

TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEURONOIN

FILE REPERENCE: A336624 067252.0107

CURRENT APPLICATION NUMBER: US/09/910,186A

CURRENT APPLICATION NUMBER: US/09/910,186A

PRIOR APPLICATION NUMBER: OS/611,419

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-07-06

PRIOR PLING DATE: 2000-05-12

PRIOR PLING DATE: 1999-05-12

PRIOR APPLICATION NUMBER: 60/133,865

PRIOR PLING DATE: 1999-05-12

PRIOR APPLICATION NUMBER: 60/133,866

PRIOR PLING DATE: 1999-05-12

PRIOR PLING DATE: 1999-05-12

PRIOR PLING DATE: 1999-05-12

PRIOR PLING DATE: 1999-05-12

PRIOR PLING DATE: 1999-05-12

PRIOR PLING DATE: 1999-05-12

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PRIOR PRIOR DATE: 1999-05-12

PRIOR PRIOR DATE: 1999-05-12
                                                                  Indels
      100.0%; Score 2288; DB 2;
100.0%; Pred. No. 1.2e-154;
ive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
Query Match
Best Local Similarity 100.
Matches 431; Conservative
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WESOUR 3

WESOUR 3

Sequence 34, Application US/09910186A

Publication No. USZ0030009025A1

GENERAL INFORMATION:

APPLICANT: U.S. Army Medical Research & Material Command

TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM

TITLE OF INVENTION: NECROMBINANT VACCINE AGAINST BOTULINUM

TITLE OF INVENTION: NECROMBINANT VACCINE AGAINST BOTULINUM

TITLE OF INVENTION: NECROMBINANT VACCINE AGAINST BOTULINUM

FILE REFERENCE: A33626-A 667252.0107

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2000-05-12

PRIOR PILING DATE: 1999-05-12

PRIOR PRILING DATE: 1999-05-12

PRIOR PILING DATE: 1999-05-12
                                                                                                                                                                                   Indels
                                                                                                     Query Match
100.0%; Score 2288; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2e-154;
Matches 431; Conservative 0; Mismatches 0;
; OTHER INFORMATION: Synthetic Construct
US-09-910-186A-16
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                                                                                                                                                    240
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                                                                                                    182 NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP 241
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                              GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 121
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GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
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100.0%; Pred. No. 1.9e-154;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Sutton, John
TITLE OF INVENTION: Constructs for Delivery of
FILE REPERENCE: 1581.092000
CURRENT APPLICANTION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
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SEQ ID NO 8
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Matches 431; Conservative
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APPLICANT: Maksymowych, Andrew
TITLE O: INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-9601
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; Pred. No. 1.2e-154;
0; Mismatches 0;
                                                                                                                    100.0%; Score 2288; DB 3;
100.0%; Pred. No. 1.2e-154;
ive 0; Mismatches 0;
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CURRENT FILING DATE: 2003-06-02
CURRENT FILING DATE: 60/384,949
PRIOR PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 188
                                                              OTHER INFORMATION: Synthetic Construct
US-09-910-186A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 178, Application US/10452024
Publication No. US20040013687A1
GENERAL INFORMATION:
APPLICANT: Simpson, Lance
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        TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 431, Conservative
                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 431; Conservative
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; OTHER INFORMATION: thrombin linker, diphtheria toxin translocation domain, BoNT/F-HU
US-10-478-516-6
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Sequence 6, Application US/10478516;
Publication No. US20040208889A1
GENREAL INFORMATION:
APPLICANT: Sutton, John M.
TILLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.1000000
CURRENT APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
ILBNGTH: 657
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US-10-478-516-5

i Sequence 5, Application US/10478516

i Bequence 5, Application US/10478516

i Bequence 5, Application No. US2004020889A1

i GENERAL INFORMATION:

APPLICANT: Sutcon, John M.

APPLICANT: Sutcon, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

FILE REFERENCE: 1581.1000000

CURRENT FILING DATE: 2003-11-24

PRIOR APPLICATION NUMBER: US/10/478,516

PRIOR PLIING DATE: 2003-11-24

PRIOR PLIING DATE: 2001-05-21

PRIOR PLIING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 32

SEQ ID NOS: 45

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US-10-478-516-5
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APPLICANT: Sutcon, John
APPLICANT: Sutcon, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR PLILING DATE: 2002-10-20
PRIOR PLILING DATE: 2000-12-04
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR PLILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING PARE: 1999-12-02
PRIOR FILING PARE: 1999-12-03
PRIOR FILING PARE: 1999-12-03
PRIOR FILING PARE: 1999-12-03
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; Pred. No. 2e-154;
0; Mismatches 0
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR FILING DATE: 2000-12-04
PRIOR PAPLICATION NUMBER: GB 9928530.6
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: synthetic construct US-10-130-973A-7
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Best Local Similarity 100.0
Matches 431; Conservative
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US-10-130-973A-4
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US-10-478-516-7
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Publication No. US20030147895A1
GENERAL INFORMATION
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GENERAL INFORMATION
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GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Sulten, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130, 973A
CURRENT FILING DATE: 2002-10-21
                                                                                                                                                   Secreted Bacterial Effector Proteins
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100.0%; Score 2288; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.9e-154;
Matches 431; Conservative 0; Mismatches 0;
                             Sequence 7, Application US/10478516
Fublication No. US20040208889A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sutton, John M.
APPLICANT: Sutton, John M.
TITLE OF INVENTION: Pharmaceutical Use of SecTITE REFERENCE: 1581.100000
CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT FILING DATE: 2003-11-24
PRIOR PILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-05-24
PRIOR PILING DATE: 2001-05-24
SUMBER OF SEG ID NOS: 32
SOFTWARE: Patentin Version 3.1
SEG ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial sequence
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yequence 26, Application US/10478516

publication No. US2004020889A1

GENERAL INFORMATION:

APPLICANT: Sthone, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

TITLE OF INVENTION NUMBER: US/10/478,516

CURRENT FILING DATE: 2002-05-21

PRIOR FILING DATE: 2002-05-24

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 32

SOSTWARE: Patentin version 3.1

SEQ ID NO 26

TITLE BENEAUTH OF SEQ ID NOS: 32

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OTHER INFORMATION: domain, with BONI/F-HC
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  Score 2288; DB 4;
Pred. No. 2.7e-154;
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100.0%; Pred. No. 3.1e-154;
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  Query Match
Best Local Similarity 100.0%;
Matches 431; Conservative 0
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Matches 431; Conservative
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Sequence (A. Application US/10130973A);
Publication No. US20030147895A1

GENERAL INFORMATION:

APPLICANT: Shone, Clifford

APPLICANT: Stiman, Nigel

TITLE OF INVENTION:

FILE REFERENCE: 1581.092000

CURRENT FILING DATE: 2002-10-21

FRICK RAPITCATION NUMBER: US/10/130,973A

CURRENT FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

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100.0%; Pred. No. 2.6e-154;
ive 0; Mismatches 0;
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                                                                                                                                  ) OTHER INFORMATION: synthetic construct US-10-130-973A-4
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                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 431; Conservative
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US-10-130-973A-6
SEQ ID NO 4
LENGTH: 862
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APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
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100.0%; Score 2288; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.5e-154;
Matches 431; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR PILING DATE: 2000-12-04
PRIOR PILING DATE: 2000-12-04
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-13-07
PRIOR FILING DATE: 1999-13-07
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/10130973A Publication No. US20030147895A1 GENERAL INFORMATION:
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; Pred. No. 3.3e-154;
0; Mismatches 0;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 1032
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Matches 431; Conservative
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Job time : 173.5 secs
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OTHER INFORMATION: diphtheria toxin translocation domain, with BONT/F-HC
US-10-478-516-23
                                                                                                                                                                                                                                                                              APPLICANT: Sutton, John M.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.1000000
CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT APPLICATION NUMBER: US/10/478,516
PRIOR APPLICATION NUMBER: PZ/5802/02384
PRIOR APPLICATION NUMBER: GB 0112687.9
PRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
1022 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 1081
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ORGANISM: Artificial sequence
                                                                                                     1082 FISKEHGWQEN 1092
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Search completed: March 2, 2006, 01:17:47

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March 2, 2006, 01:12:18; Search time 17.5 Seconds (without alignments) 491.279 Million cell updates/sec Run on:

US-08-981-087B-1 2288 1 SYTNDKILILYFNKLYKKIK......TSSNGCFWSFISKEHGWQEN Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

133702 segs, 19947517 residues Searched: 133702 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Cgn2 6/ptodata/1/pubpaa/USO8\_NBW\_PUB.pep:\*
/cgn2 6/ptodata/1/pubpaa/USO6\_NBW PUB.pep:\*
/cgn2 6/ptodata/1/pubpaa/USO7\_NBW PUB.pep:\*
/cgn2 6/ptodata/1/pubpaa/USO7\_NBW PUB.pep:\*
/cgn2 6/ptodata/1/pubpaa/USO9\_NBW PUB.pep:\*
/cgn2 6/ptodata/1/pubpaa/USI0\_NBW PUB.pep:\*
/cgn2 6/ptodata/1/pubpaa/USI1\_NBW PUB.pep:\*
/cgn2 6/ptodata/1/pubpaa/USI1\_NBW PUB.pep:\* Published\_Applications\_AA\_ Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		,			SUMMERTES	
Result No.	Score	Query Match	* Query Match Length	DB	ΔI	Description
-	2288	100.0	1059	7	US/11/062	Sequence 5, Appli
7	2288	100.0	1084	7	US/11/062	Sequence 8, Appli
ক্র	1833	80.1	838	φ	US-10-909-769-28	
3	1457.5	63.7	829	9	US-10-909-769-26	26,
'n	1120.5	49.0	849	ø	US-10-909-769-18	
9	1120.5	49.0	1067	7	US/11/062	Sequence 3, Appli
7	4,120.5	49.0	1092	7	US/11/062	Sequence 6, Appli
00	781	34.1	900	9	US-10-909-769-20	Sequence 20, Appl
σ	769	33.6	1070	7	US/11/062	Sequence 4, Appli
10	769	33.6	1095	7	US/11/062	Sequence 7, Appli
11	736.5	32.2	855	9	US-10-909-769-30	Sequence 30, Appl
12	676.5	29.6	1169	7	US-11-077-550-20	Sequence 20, Appl
13	580.5	25.4	834	9	US-10-909-769-24	Sequence 24, Appl
14	553	24.2	1315	7	US-11-077-550-141	141
15	546	23.9	842		US-10-909-769-22	22, A
16	160	7.0	588	7	US-11-052-554A-339	339
17	149.5	6.5	2340	7	US-11-052-554A-171	Sequence 171, App
18	147	6.4	2710	7	US-11-051-453-41	Sequence 41, Appl
19	135	5.9	2902	7	US-11-052-554A-91	Sequence 91, Appl
20	129	5.6	2367	7	US-11-051-453-42	Sequence 42, Appl
21	126	5.5	874	7	US-11-087-099-10263	Sequence 10263, A
22	125.5	5.5	849	7	US-11-087-099-1756	Sequence 1756, Ap
23	125.5	5.5	3194	7	US-11-052-554A-90	Sequence 90, Appl
24	125	5.5	871	7	US-11-087-099-6053	Sequence 6053, Ap
25	120	5.2	267	9	US-10-485-517-216	Sequence 216, App

Sequence 351, App Sequence 1, Appli Sequence 1, Appli Sequence 83, Appl Sequence 92, Appl Sequence 128, Appl Sequence 126, Appl Sequence 126, Appl Sequence 130, Appl Sequence 122, Appl Sequence 122, Appl Sequence 122, Appl Sequence 122, Appl Sequence 123, Appl Sequence 126, Appl Sequence 126, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 164, Appl Sequence 11042, Appl Sequence 11
US-10-485-517-351 US-11-052-554A-1 US-11-052-554A-82 US-11-052-554A-82 US-11-052-554A-92 US-11-131-479-22 US-11-131-479-22 US-11-077-550-126 US-11-077-550-126 US-11-077-550-126 US-11-077-550-126 US-11-077-550-127 US-11-077-550-127 US-11-077-550-128 US-11-077-550-128 US-11-077-550-129 US-11-077-550-129 US-11-077-550-129 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128 US-11-077-550-128
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## ALIGNMENTS

<u>.</u>		TYPE: PRT ORGANISM: Artificial Sequence PRATURE: OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilu 1/062,471A-5	Gaps
ULT 1 11/06c 5, Application US/11062471A equence 5, Application US/11062471A ublication No. US20050255093A1 ENERAL INFORMATION: ENERAL INFORMATION: APPLICANT: SUTTON, John Mark APPLICANT: HALLIS, Bassam APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, Nigell APPLICANT: SILMAN, SILMAN, SILMAN		earoth.	100.0%; Score 2288; DB 7; Length 1059; 100.0%; Pred. No. 3.4e-160; tive 0; Mismatches 0; Indels 0;
9 2 4		B. st	Length
		from	7; 1 160; 0;
		n-sob	, DB 3.4e- es
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171A les	TITIES OF INVENTION: DELIVELY OF SUPERCONDERING OF THE STEERENCE: 1581.0800001 CURRENT APPLICATION NUMBER: US/11/062,471A CURRENT FILING DATE: 2005-02-22 PRIOR APPLICATION NUMBER: 09/831,050 PRIOR FILING DATE: 1999-11-05 PRIOR FILING DATE: 1999-11-05 PRIOR FILING DATE: 1999-11-05 PRIOR PLING DATE: 1999-11-05 PRIOR FILING DATE: 1999-11-05 PRIOR FILING DATE: 1999-11-05 PRIOR FILING DATE: 1999-11-05 PRIOR PLING DATE: 1999-11-05 PRIOR DATE: 1999-11-05 PRIOR DATE: 1999-11-05	омргів	Score Pred. 0, Mis
ULT 1 11/062 equence 5, Application US/11062471. ublication No. US20050255093A1 ENERAL INFORMATION: ENERAL INFORMATION: APPLICANT: SHONE, Clifford Charles APPLICANT: HALLIS, Bassam APPLICANT: SILMAN, Nigel	TITLE OF INVENTION: DELIVETY OF SUPPERING STRENGE: 1581.0800001 CURRENT APPLICATION NUMBER: US/11/06 CURRENT FILING DATE: 2005-02-2 PRIOR PELING DATE: 1999-11-05 PRIOR APPLICATION NUMBER: OF/GB99/0 PRIOR APPLICATION NUMBER: GB 9824282 PRIOR FILING DATE: 1999-11-05 PRIOR APPLICATION NUMBER: GB 9824282 PRIOR FILING DATE: 1999-11-05 SUPTHARE: PALENTIN NUMBER: GB 9824282 SUPTHARE: PALENTIN VOMBER: GB 9824282 SOFTWARE: PALENTIN VOMBER: GB 9824282 SOFTWARE: PALENTIN VOMBER: GB 9824282 SOFTWARE: PALENTIN VOMBER: GB 9824282	ence uct c	, 0, %; 0, %;
pplication US/110 o. US20050255093A MATION: HONE, Clifford Ch SUTTON, John Mark HALLIS, Bassam STILMAN, Nigel	TITLE OF LAVENILOR: DELICATY CURRENT APPLICATION NUMBER: U CURRENT FILING DATE: 2005-02 PRIOR FILING DATE: 1999-11-05 PRIOR APPLICATION NUMBER: 9CT PRIOR FILING DATE: 1999-11-05 PRIOR APPLICATION NUMBER: PCT PRIOR APPLICATION NUMBER: GB PRIOR FILING DATE: 1999-11-05 SPRIOR FILING DATE: 1999-11-05 SOFTWARE: PCT SOFTWARE: PALENTIN VOY: 2.1 EQ. ID NOS: 11 LENGTH: 1059	TYPE: PRT ORGANISM: Artificial Sequence PRATURE: OTHER INFORMATION: CONSTRUCT 1/062,471A-5	ø
pplication US o. US20050255 MATION: HONE, Cliffor SUTTON, John HALLIS, Bassa SILMAN, Nigel	TITIES OF INVENTION: DELLIFIES OF INVENTION: DELLIFIES OF CURRENT APPLICATION NUMBERORS APPLICATION NUMBER PRIOR FILING DATE: 1999-PRIOR PRIDRE OF SEQ ID NOS: 11 NUMBER OF SEQ	ficia ION: (	Query Match Best Local Similarity Matches 431; Conserv
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RESULT 1 US/11/062 5. Application US/11062471A Sequence 5. Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION: APPLICANT: SHONE. Clifford Charles APPLICANT: SUTTON, John Mark APPLICANT: SILMAN, Nigel APPLICANT: SILMAN, Nigel	FILLE CURRI CURRI PRIOI PRIOI PRIOI PRIOI NUMBI SCO II	TYPE: PRT ORGANISM: Ar. PEATURE: OTHER INFORM US/11/062,471A-5	Query Best Match
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NLIDEKSISNLGDIHVSDNILFKIVGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDP

181 809

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GENERAL INFORMATION

APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei Roger
APPLICANT: Aoki, Kei Roger
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLE0010-100 (ROI2003-146)
CURRENT FILING DATE: 2044-08-02
NUMBER OF SEQ ID NOS: 34
SSC IND NOS: 34
SSC IND NO 28
LENGTH: 838
EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 1013
                                                            1014 NSLGQIIVMDSIGNNCTWAFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 1073
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                                  NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS
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80.1%; Score 1833; DB 6; I
Best Local Similarity 81.3%; Pred. No. 6e-127;
Matches 352; Conservative 33; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-28
                                                                                                                                                                                                                            Sequence 28, Application US/10909769
Publication No. US20060024331A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                                                       989 NSLGQIIVMDSIGNNCTMNFQNNNGGNIGLIGFHSNNLVASSWYNNIRKNTSSNGCFWS 1048
                                                                              EVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSN 360
                                                                                                     NSLGQIIVMDSIGNNCTWNPQNNNGGNIGLLGFHSNNLVASSWYYNNIRKNTSSNGCFWS 420
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                                                                                                                                                                                                                                                                                                                                                                       FULICATION NO. USJOURNATION:
APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE APPLICATION DELIVERY OF SUPERIOR DISMUTASE TO NEURON THE COURSENT PILING DATE: 1980-001
CURRENT FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATCHTIN VOWER: GB 9824282.9
NUMBER OF SEQ ID NOS: 11
SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                              ' Sequence 8, Application US/11062471A
' Publication No. US20050255093A1
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ORGANISM: Artificial Sequence
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APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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                                                                                                                                                                                                                                      Length 849;
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                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.4%; Pred. No. 1.1e-74;
Matches 219; Conservative 78; Mismatches 127;
                                                                                                                                                                    ; OTHER INFORMATION: Amino acid sequence of HC
US-10-909-769-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 IRKNTSSNGCFWSFISKEHGWQE 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHONE, Clifford Charles
                               2004-08-02
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                                                   NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 18
EBNCTH: 849
                                                                                                                           TYPE: PRT
ORGANISM: Artificial Seguence
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SOFTWARE: PatentIn Ver.
                                 CURRENT FILING DATE:
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APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Lin, Wei-Jen

APPLICANT: Sachs, Kei Roger

APPLICANT: Sachs, George

TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist;
FILE REFERENCE: ALLEGO10-100 (ROIZ003-146)

CURRENT APPLICATION NUMBER: US/10/909,769

CURRENT FILING DATE: 2004-08-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.3

SEQ ID NO 26

LENGTH: 829

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APPLICANT: Lin, Wei Jen
APPLICANT: Lin, Wei Jen
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.7%; Score 1457.5; DB 6; 63.4%; Pred. No. 2e-99; iive 72; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Amino acid sequence of HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ALLEGO110-100 (RO12003-146) CURRENT APPLICATION NUMBER: US/10/909,769
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Publication No. US20060024331A1
GENERAL INFORMATION
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
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GCFWNFISEEHGWOE 828
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APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Lin, Wei-Jen APPLICANT: Lin, Wei-Jen APPLICANT: Aoki, Kei Roger APPLICANT: Sachs, George TITLE OF INVENTUAN: Toxin Compounds with Enhanced Membrane Translocation Characteris FILE REFERENCE: ALLEO10-100 (RO12003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                   118 NSGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIY 177
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                               61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNN
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                                                                                       62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW
                                                                                                                                                                     122 KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Amino acid sequence of HC US-10-909-769-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 IRKNTSSNGCFWSFISKEHGWQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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174; Conservat
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Best Local
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; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker.
US/11/062,471A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION's Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION's Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION's Delivery of Superoxide Dismutase to Neuronal Cells
CURRENT PELLING DATE: 1991.080001
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                LIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFDTBLGKTEIETLYSDEPDP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 SILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 SNSNNSLGQIIVMDS----IGNNCTMNPQNNNGGNIGLLGFHSNN----LVASSWYYNN 407
                                                                                                                                                                                                                                                                                                                     KISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGN 181
                                                                                                                                                                                                                                        IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
                                                                                                                                                         2 YTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
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49.4%; Pred. No. 1.4e-74;
ive 78; Mismatches 127; Indels 19;
                                                                          Length 1067;
                                                                                                                    19;
                                                                      ; Score 1120.5; DB 7; Length
; Pred. No. 1.4e-74;
78; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRKNISSNGCFWSFISKEHGWQE 430
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                                                                              49.0%;
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Best Local Similarity 49.43
Matches 219; Conservative
                                                                                                                      Conservative
                                                                            Query Match
Best Local Similarity
Matches 219; Conserv
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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human N
US/11/062,471A-7
                                                                                                                                                 962 YKYFKKEBEKLFLAPISDSDBFYNTIQIKEYDEQPTYSCQLLFKKDERSTDEIGLIGHR 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSDE 237
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                                                                                                                   341 DISIAKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNPQNN--NGGNIGLLGFH- 394
858 SYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNŚKYINYRD 917
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                                      281 ORGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYA
                                                                APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         903
                                                                                                                                                                                                                              PYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGCNWQFIPKDEGWTE 1070
                                                                                                                                                                                                      -----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWOE 430
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ilarity 36.0%; Pred. No. 8.5e-49;
Conservative 88; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: 09/831,050
PRIOR FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 1581.0800001
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 7
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Best Local Similarity
Matches 169; Conserve
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US/11/062,471A-4
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                                                                                                                                                                                                                 APPLICANT: SHONE, CLIfford Charles
APPLICANT: SHONE, CLIfford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE REFERENCE: 1581.0800001
CURRENT PELLING NUMBER: US/11/062,471A
CURRENT PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
                                                     280 QQRGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLY 339
                             INGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSD 236
                                                                                                          EPDPSILKDFWGNYLLYNKRYYLLNL-----LRTDKSI-----TQNSNFLNIN 279
                                                                                                                                                                                                                                                                         340 ADISIAKPEKIIKLIRTSNSNNSLGQIIVM---DSIGNNCTWNFQNN--NGGNIGLLGFH 394
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33.6%; Score 769; DB 7; Length 1070;
Best Local Similarity 36.0%; Pred. No. 8.2e-49;
Matches 169; Conservative 88; Mismatches 152; Indels 6
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jenn
APPLICANT: Lin, Wei-Jenn
APPLICANT: Acki, Wei-Jenn
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REPERENCE: ALLEO10 -100 (ROIZ003-146)
CURRENT PILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
LENGTH: 855
987 XKYFKKEBEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEBSTDEIGLIGIHR 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 NGNLIDEKSISNLGDIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSDE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 IFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVD-RDVEYRLYADISIAKPE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 PDPSILKDFWGNYLLYNKRYYLLN------LLRTDKSITQNSNFLNINQQRGVYQKPN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      756 QTQLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDYGYVWD 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQ---NNNGGNIGLLGF-----
                                                                  ----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.2%; Score 736.5; DB 6; Length 35.7%; Pred. No. 1.5e-46; tive 76; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 -HSNNLVASSWYYNNIRKNTSS--NGCFWSFISKEHGWQE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Amino acid sequence of HC
                                                                                                                                                   Sequence 30, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
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US-11-077-550-20
Sequence 20, Application US/11077550
Publication No. US20050244435A1
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.7%
Matches 164; Conservative
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Acki, Kei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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GENERAL INFORMATION:

APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Coter, Keith Alan
APPLICANT: Coter, Keith Alan
APPLICANT: Coter, John
APPLICANT: Catedock, John
APPLICANT: Statcon, J. Mark
APPLICANT: Statcon, J. Mark
APPLICANT: Statcon, J. Mark
APPLICANT: Recombinant Toxin Fragments
FILE REFERENCE: 1501.0130004
CURRENT FILING DATE: 2005-03-11
FILE REFERENCE: 1501.0130004
CURRENT FILING DATE: 2005-09-12
FRIOR PELICATION NUMBER: 00/255,829
FRIOR FILING DATE: 1999-02-23
FRIOR PELING DATE: 1997-08-22
FRIOR APPLICATION NUMBER: 06/255,829
FRIOR PELING DATE: 1996-12-17
FRIOR PELING DATE: 1996-12-17
FRIOR PELING DATE: 1996-12-17
FRIOR PELING DATE: 1996-12-17
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FRIOR FILING DATE: 1996-13-13
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29.6%; Score 676.5; DB 7
Best Local Similarity 40.6%; Pred. No. 5.5e-42;
Matches 141; Conservative 66; Mismatches 99
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Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Clostridium botulinum US-11-077-550-20
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US-10-909-769-24
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OTHER INFORMATION: Amino acid sequence of HC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 VEVIIR----KNGSTDISNTDNFVRK---NDLAYINVVDRDVEYRLYADISIAKPEKIIK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 SYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVGDNVQLNTIYTNDF 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 LIRTSNSNNSLGQIIVMDSIGNNCTMNF----QNNNGGNIGLLGFHSNNLVASSWY--- 404
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                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                             Query Match 25.4%; Score 580.5; DB 6; Length 834; Best Local Similarity 29.4%; Pred. No. 4e-35; Matches 140; Conservative 88; Mismatches 156; Indels 93
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APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
CURRENT APPLICATION NUMBER: US/10/909,769; CURRENT APPLICATION NUMBER: US/10/909,769; CURRENT FILLING DATE: 2004-08-02; NUMBER OF SEQ ID NOS: 34; SOFTWARE: Patentin version 3.3; SEQ ID NO 24; LENGTH: 834
                                                                                                                                                                                                          ; OTHER INFORMATION: Amino acid seqence of HC US-10-909-769-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE PEFERENCE: 1591.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
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PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: PCT/GB97/02273
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 141, Application US/11077550
Publication No. US20050244435A1
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PRIOR FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
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Stancombe, Patrick
                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Marks, Philip
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APPLICANT:
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Wei-Jen
APPLICANT: Aoki, Kei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLE0010-100 (R012003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1218 FNNLDRIL---RVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQ 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLN----INQQRGVYQKPNIFSNTRLYTG
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                                                                                                                                                                                                                                                                                                                                                         Length 1315;
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1275 IGNDPNRDILIASNWYFNHLKDKIL--GCDWYFVPTDEGW 1312
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                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 553; DB 7; 30.2%; Pred. No. 7.2e-33;
                     PRIOR FILING DATE: 1996-12-27
PRIOR APPLICATION NUMBER: GB962596.5
PRIOR FILING DATE: 1996-12-13
PRIOR PRILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PATCHTIN VERSION 3.1
SEQ ID NO 141
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APPLICATION NUMBER: 08/782,893
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Publication No. US20060024331A1
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                                                                                                                                                                                                                                                                                ORGANISM: Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fernandez-Salas,
                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 30.2
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           US-11-077-550-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-909-769-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398
                                                                                                                                                                                                                                                                                                                                                              Query Match
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US-10-909-769-22

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179 NGNLIDEKSISNLGDIHVSDNILFKIVGCNDTRYV------GIRYFKVFDTELGKTE 229
                                                                                                                                                                                                        576 NGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNINMIRDFYIFAKELDGKD 635
                                                                                                                                                                                                                                        230 IETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNFLNINQQRGVYQKPN 289
                                                                                                                                                                                                                                                    290 IFSNIRLYIGVEVIIRK-NGSIDISNIDNFVRKNDLAYINVVDRDVEYRL-----YAD 341
                                                                                                                                                                                                                                                                                                     743 NHSTEDIYALGLREQTKDI------NDNIIFQIQPMNNTYYYASQIFKSNFNGENISGI 795
                                                                                                                                                                                                                                                                                                                                     342 -----ISIAKPEKIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNN-NGGNI-GL 390
                                              1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNOF 60
                           Gaps
                           199
  23.9%; Score 546; DB 6; Length 842; 31.5%; Pred. No. 1.4e-32; Live 82; Mismatches 169; Indels
                                                                                                                                                                                                                                                                                                                                                                                   391 LGFHSNNL-VASSWYYNNIRKNTSSNGCF------WSFI 422
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.5'
Matches 146; Conservative
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Search completed: March 2, 2006, 01:18:28 Job time : 18.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein ; Search time 68.993 Seconds 2, 2006, 00:31:42 March Run on:

(without alignments) 917.057 Million cell updates/sec

US-08-981-087B-2 770 1 SYTNDKILLILYFNKLYKKIK..........LNYNKIIWTLQDTAGNNQKL 144 Perfect score:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Sequence:

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s Geneseq 21:\* 9:::9 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:

#### SUMMARIES

		de			SOUTHER	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	770	100.0	144	2	AAW09015	Aaw09015 Immunogen
8	770	100.0	431	~	AAW09014	Aaw09014 Immunogen
e	77.0	100.0	432	4	AAB04103	Aab04103 Botulism
4	770	100.0	432	4	AAB04096	
Ŋ	770	100.0	645	4	AAE07894	_
9	770	100.0	645	9	AAE35692	Aae35692 DipT HN d
7	770	100.0	657	9	AAE35693	Aae35693 BONT/F-Hc
8	770	100.0	657	ø	AAE35694	Aae35694 BoNT/F-Hc
6	770	100.0	099	4	AAE07898	Aae07898 Modified
10	770	100.0	685	4	AAE07893	
11	770	100.0	862	4	AAE07890	Aae07890 Modified
12	770	100.0	887	4	AAE07892	Aae07892 Modified
13	770	100.0	979	9	AAE35713	Aae35713 BONT/F-Hc
14	770	100.0	1032	4	AAE07901	Aae07901 C. botuli
15	770	100.0	1059	ო	AAY93309	Aay93309 A mangane
16	770	100.0	1084	m	AAY93312	A
17	770	100.0	1092	4	AAE07900	Aae07900 C. botuli
18	770	100.0	1192	9	AAE35711	Aae35711 BONT/F-HC
19	770	100.0	1192	9	AAE35710	Aae35710 BoNT/F-Hc
20	767	99.6	432	m	AAY77138	Aay77138 Synthetic
21	593.5	77.1	448	7	AAW68399	Aaw68399 Clostridi
22	568.5	73.8	451	~	AAW68395	Aaw68395 Clostridi
23	565.5	73.4	449	ო	AAY77137	Aay77137 Synthetic
24	565.5	73.4	449	4	AAB04094	Aab04094 Botulism

Aaw68396 Clostridi	Aab04095 Botulism	Aay77140 Native bo	Aab04081 Botulism	Adz69764 Botulinur	Aay93307 A mangane	Aay93310 A mangane	Aar95010 C. botul	_	_	_	Adz69730 Botulinum	Adz69729 Clostridi	Adz69831 Inactive	Ad192142 Clostrid	Aau99339 Clostrid	Aay77143 Botulinum	Aay77142 Native bo	_	Aar95008 Type A ne	. T. 1410([] 0000)«
AAW68396	AAB04095	AAY77140	AAB04081	ADZ69764	AAY93307	AAY93310	AAR95010	ADW11038	ADZ36018	ADZ60275	ADZ69730	ADZ69729	ADZ69831	ADL92142	AAU99339	AAY77143	AAY77142	AAB04088	AAR95008	00000000
7	4	٣	4	6	ო	m	7	6	σ	σ	6	σ	σ	œ	Ŋ	٣	m	4	7	c
452	419	837	847	859	1067	1092	1296	1296	1296	1296	1296	1302	1302	848	1295	233	432	437	438	0.57
72.9	8.69	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.2	49.0	48.4	48.2	48.2	48.2	48.2	0 7
561.5	537.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	378.5	377.5	372.5	371.5	371.5	371.5	371.5	27.7
25	56	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4

## ALIGNMENTS

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Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant
                                                                                                                                                                                                                        Botulinum toxin; neurotoxin; BoBI/F; immunogen; vaccine; botulism.
                                                                                                                                                                          Immunogenic type F botulinum toxin polypeptide (aa848-991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasechnik VA;
                                                                                                                                                                                                                                                                     Clostridium botulinum; type F strain Langeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elmore MJ, Mauchline ML, Minton NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROBIOLOGICAL RES AUTHORITY
                  AAW09015 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            95GB-00011909.
                                                                                                                                    (first entry)
                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-065467/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-1995;
                                                                                                                                                                                                                                                                                                                       WO9641881-A1
                                                                                                                                                                                                                                                                                                                                                                 27-DEC-1996.
                                                                                                             17-OCT-2003
31-MAR-1997
                                                                  AAW09015;
AAW09015
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Claim 5; Page 17-18; 37pp; English.

Novel polypeptides (AAM09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BoNT/F). They lack the Lotain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine produced Recombinant polypeptides can be produced in transformed host cells, as fusion proteins, e.g. with malcose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 144 AA;

Query Match

100.0%; Score 770; DB 2; Length 144;

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                                                                                                                  GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                    GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNFYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278) of a type F botulinum neurotowin (powm/p)
                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of a type F botulinum neurotoxin (BoNT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAM09015-17) lack the light chain and MN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin, making them useful for vaccine produ. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                                          1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                       1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; botulism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 431;
                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic type F botulinum toxin heavy chain (aa848-1278).
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasechnik VA;
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 770; DB 2;
100.0%; Pred. No. 1.7e-68;
ive 0; Mismatches 0;
               Pred. No. 4.2e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                 BoBT/F; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum; type F strain Langeland
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elmore MJ, Mauchline ML, Minton NP,
                                                                                                                                                                                                 121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                             121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 16-17; 37pp; English.
                                                                                                                                                                                                                                                                                  AAW09014 standard, protein, 431 AA.
100.0%; PAL
                                                                                                                                                                                                                                                                                                                                                                                                                   Botulinum toxin; neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-GB001409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95GB-00011909
                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 144; Conservative
             Best Local Similarity 100.
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-065467/06.
N-PSDB; AAT48100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                          17-OCT-2003
31-MAR-1997
                                                                                                                                                                                                                                                                                                              AAW09014;
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Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a clisulfide bond. Nucleic acide encoding the carboxy-terminal (HC) or amino terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acide are expressible in a recombinant corpanisms such as Escherichia coli or Pichla pastoris. The use of recombinant nucleic acide are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium.

Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acide can be derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                  61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANEYTIIDCIRNNNSG 120
 120
GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
                                                                                                                                                                                                                                                                                                                                  Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith LA, Byrne MP, Middlebrook JL, Lapenotiere H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                      WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 18b; 73pp; English.
                                                                                                                                                                                              ¥.
                                                                                                                                                                                              AAB04103 standard; protein; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0133865P.
99US-0133866P.
99US-0133867P.
99US-0133868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAY-2000; 2000WO-US012890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0133873P
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-016048/02.
N-PSDB; AAA54499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against botulism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200067700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                               11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1999
12-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                       infection
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                      121
 61
                                                                                                                                                                                                                               AAB04103;
                                                                                                                                                          RESULT 3
                                                                                                                                                                            AAB04103
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Score 770; DB 4; Length 432; Pred. No. 1.7e-68;

100.0%;

Query Match Best Local Similarity

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Gaps

; 0

Indels

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SYTNDKILILYFNKLYKKIKDNSILDMRYENNKRIDISGYGSNISINGDVYIYSTNRNQF

SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF

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Length 432; IndelB 9 61

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial neurotoxin and is not a fragment or derivative of useful for the treatment of a disease state associated with neuronal cells. The puppetide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                     GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                              62 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIFKYFNKVNLNNEYTIIDCIRNNNSG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BoMT/F.
                                                                                                                                                                                                   2 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                               ; Score 770; DB 4;
; Pred. No. 1.7e-68;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified clostridial heavy chain fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                           WKISLNYNKIIWTLQDTAGNNQKL 145
Clostridium botulinum serotypes A-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE07894 standard; protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
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                                                                                      100.08;
                                                                                                      Best Local Similarity 100.0%;
Matches 144; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shone CC, Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514643/56.
                                             Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-2003
01-NOV-2001
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                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Eschérichia coli or Pichia pastoris. The use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from
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                                                                                                                                   GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                        9
                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids encoding the carboxy- or amino-terminal portions of theavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                               1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                          2 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Botulism toxin heavy chain C-terminal sequence (serotype F)
         0; Indels
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         0; Mismatches
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                                                                                                                                                                                                                                                     122 WKISLNYNKIIWTLQDTAGNNQKL 145
                                                                                                                                                                                                                       WKISLNYNKIIWTLODTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                  AAB04096 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 9b; 73pp; English.
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99US-0133867P.
99US-0133868P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
           Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-016048/02.
N-PSDB; AAA54490.
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Synthetic

Smith LA,

us-08-981-087b-2.rag

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 and infection. They are also useful in gene therapy. The present sequence is a modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain of botulinum neurotoxin type F (BONT/F) with translocation domain of diphtheria neurotoxin. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                   GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                                                     275 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; Prion disease, Alzheimer' disease; hypersecretion disorder; muscle spasm; ODD; Dronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; translocation domain, HN domain; DipT; HC; botulinum type F neuroboxin;
                                                                                                                                                                                                          215 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                    1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder
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                                                                                                                                Length 645;
                                                                                                                                                            Indels
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                                                                                                                         100.0%; Score 770; DB 4;
100.0%; Pred. No. 2.9e-68;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DipT HN domain-BoNT/F-Hc fusion construct.
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                                                                                                                                                                                                                                                                                                                 WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                   WKISLNYNKIIWTLQDTAGNNQKL 358
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                                                                                                                                                                                                                                                                                                                                                                                                                         AAE35692 standard; protein; 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2002; 2002WO-GB002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium diphtheriae.
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                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 144, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding domain; BoNT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ostridium botulinum,
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                                                                                             Sequence 645 AA;
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for treatment selected from proming or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory

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mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular tracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating prion disease, Alzheimer, disease and wide range of disorders inhibiting secretion disorders such as blephorospasm, torticolls and hypersecretion disorders such as blephorospasm, torticolls and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and aschma. The present sequence is a fusion construct comparising Corynebacterium diphtheria diphtheria toxin translocation domain (Dip-HN domain) and botulinum type F neurotoxin from Clostridium botulinum. This sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNIANEYTIIDCIRNNNSG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis, therapy, inflammatory mediator; intracellular trafficking, infection, Prion disease, Alzheimer' disease, hypersecretion disorder; muscle spasm, COPD, bronchitis; chronic obstructive pulmonary disease, torticolis, blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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100.0%; Pred. No. 2.9e-68;
ive 0; Mismatches 0;
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sutton JM, Shone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 645 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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(MICR-) MICROBIOLOGICAL RES AUTHORITY.

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking secretion from cells. The invention is also useful for treating prion disease, Alzheimer' disease and wide range of disorders including muscle spaems such as blephorospasm, torticolis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HW domain), botulinum type F neurotoxin binding domain (BONT/F-Hc) from Clostridium botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention
                        Example 12; Page 60-63; 130pp; English
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100.0%; Score 770; DB 6; Length 657; 100.0%; Pred. No. 3e-68; ive 0; Mismatches 0; Indels C WKISLNYNKIIWTLODTAGNNOKL 144 Matches 144; Conservative Query Match Best Local Similarity Sequence 657 AA; 61 121 유 ઠે 셤 ठ 뭐

(first entry) 17-JUN-2003 AAE35694; RESULT 8 **AAE35694** 

infection; Prion disease, Alzheimer' disease; hypersecretion disorder; muscle appasm; ODDP, bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; boNT/F; translocation domain; HN domain; DipT; Hc; binding domain; Apoptosis; therapy; inflammatory mediator; intracellular trafficking;

Corynebacterium diphtheriae. botulinum type F neurotoxin Clostridium botulinum. Unidentified.

WO200296467-A2. Chimeric.

05-DEC-2002

21-MAY-2002; 2002WO-GB002384.

24-MAY-2001; 2001GB-00012687.

ö 286 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 287 GIYSSKPSEVUIAQNNDIIYNGRYQNFSISFWVRIPKYFPKNFNNLNNEYTIIDCIRNNNSG 346 9 227 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF Gaps .. 0 347 WKISLMYNKIIWTLQDTAGNNQKL 370

BoNT/F-Hc-DipT HN domain-factor Xa linker fusion construct. AAE35694 standard; protein; 657 AA

The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for medulating expression of cells sufface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including mancle spasms such as blephorospasm, toritionis and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HW domain). Notulinum type F neurotoxin binding domain (BONT/F-HC) from Clostridium botulinum and factor Xa linker peptide. This sequence is used in the exemplification of the invention 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell. 1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF ö 100.0%; Score 770; DB 6; Length 657; 100.0%; Pred. No. 3e-68; ö Modified clostridial heavy chain fragment #5. 0; Mismatches Example 12; Page 63-65; 130pp; English. 347 WKISLNYNKIIWTLQDTAGNNQKL 370 WKISLNYNKIIWTLQDTAGNNOKL 144 AAE07898 standard; protein; 660 AA (first entry) Query Match
Best Local Similarity 100.
Matches 144; Conservative (revised) WPI; 2003-167247/16. Sequence 657 AA; 11-SEP-2003 01-NOV-2001 Sutton JM, AAE07898; 121 AAE07898 RESULT В 셤 ઠે 엄 8 ò

286

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tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; tetanus neurotoxin; TeNT; botulinum neurotoxin type F; BONT/F. Corynebacterium diphtheriae Clostridium tetani. Clostridium botulinum. Chimeric us-08-981-087b-2.rag

Geobacillus stearothermophilus

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a MN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the constructed processor and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain which is a hybrid of botulinum neurotoxin type F (BoNT/F) and tetanus neurotoxin (Updated on 11-SEP-2003 to translocation domain of diphtheria neurotoxin. (Updated on 11-SEP-2003 to
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                                                                                                                                                                                                                                                                                                 New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; botulinum neurotoxin type F; BONT/F.
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                                                                                                                                                                              (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                        Silman N;
                                                                           04-DEC-2000; 2000WO-GB004644.
                                                                                                                                      07-APR-2000; 2000GB-00008658.
                                                                                                                   99GB-00028530
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WO200158936-A2
                                                                                                                 02-DEC-1999;
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                                     16-AUG-2001
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Best Local &
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurocxin and is not a fragment or derivative of a HN domain of a clostridial neurocxin and is not a fragment or derivative of useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours
                                                                                                                                                                                                                                                                                                                                                                                                                         New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MnSOD), from Bacillus stearothermophilus, linker that can be cleaved by factor Xa, translocation peptide from influenza virus and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BoNT/F)
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                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Page 43; 50pp; English
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07-APR-2000; 2000GB-00008658
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                   Influenza virus.
Clostridium botulinum.
Synthetic.
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                                                                                                                    WO200158936-A2
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                                                                                Chimeric.
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314

AAE07892 standard; protein; 887 AA.

(first entry)

01-NOV-2001

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (actoroxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell, where the translocation domain (amino terminal half of HC, designated as HN), that translocation domain (amino terminal half of HC, designated as HN), that translocation is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the cost influding neurodesnerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate compises bacterial hn-superoxide dismutase (MNSO), from Conjugate compises bacterial hn-superoxide dismutase (MNSO), from translocation domain from diphtheria neurotoxin and a neuronal cell-cepted present sequence translocation domain from diphtheria neurotoxin type F (BONT/F))
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                                  Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
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Modified clostridial heavy chain-superoxide dismutase conjugate #2
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al Similarity 100.0%; Score 770; DB 4;
al Similarity 100.0%; Pred. No. 4.2e-68;
144; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Silman N;
                                                                                                                                      Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
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07-APR-2000; 2000GB-00008658.
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Best Local Similarity
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the invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (Ht) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino cerminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN comain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises a mitochondrial leader sequence from human Mn-superoxide dismutase (MnSOD), MnSOD from Bacillus steadorbermophilus, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
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                                                                                                                                                                 tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
                                                                                                           Modified clostridial heavy chain-superoxide dismutase conjugate #4.
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                                                                                                                                                                                                                                                                  Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
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07-APR-2000; 2000GB-00008658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 144, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514643/56.
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                                                                                                                                                                                                                                                                                                                                                                                          WO200158936-A2
                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2001
                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shone CC,
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                                                                                                                                                                                                                                                                                                                                                     Chimeric.
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Sequence 979 AA;

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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; conjubiting survival of cells; promoting or inhibiting survival of cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells, and intracellular mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spaams such as chronic obstructive pulmonary disease comprising corpresents such as chronic obstructive pulmonary disease comprising corynebacterium diphtheriae diphtheria toxin translocation comprised comprised corpusation botulinum type F neurotoxin binding domain (BDPT-HN domain), botulinum type F neurotoxin binding domain (BDNT/F-HC) from Clostridium botulinum and factor Xa linker peptide and Yersinia peetls targetted effector protein yopT. This sequence is used in the exemplification of the invention
Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BONT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis, therapy, inflammatory mediator; intracellular trafficking; infection, Prion disease, Alzheimer' disease, hypersecretion disorder; muscle spasm, CODD, bronchitis, chronic obstructive pulmonary disease; torticolis, blephorospasm, asthma, fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; Dipf; Hc; binding domain; botulinum type F neurotoxin; targetted effector protien; Yopf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Page 110-114; 130pp; English
                                                                                                                           WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                        577 WKISLNYNKIIWTLQDTAGNNOKL 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAE35713 standard; protein; 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001GB-00012687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-2002; 2002WO-GB002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium diphtheriae. Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutton JM, Shone CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-167247/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia pestis.
Unidentified.
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                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE35713;
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                                                                                                                                                                                                                                                                                                                                         RESULT 13
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is c. botulinum C2 enterotoxin translocation domain with botulinum neurotoxin type F (BONI/F) binding domain used in the exemplification of
                                                    ö
                                                                                                                    609
                                                                                                                                                      120
                                                                                                                                                                    New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                                                  61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANEYTIIDCIRNNNSG
                                                                               1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  C. botulinum C2 translocation domain with BoNT/F-binding domain #2.
                                                   ;
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                 Length 979;
                                                   Indels
   Score 770; DB 6; r
Pred. No. 5e-68;
100.0%; Scor.
100.0%; Pred. No. o.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                121 WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                669 WKISLNYNKIIWTLQDTAGNNQKL 692
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                                                                                                                                                                                                                                                                                                                                 AAE07901 standard; protein; 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2000; 2000WO-GB004644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001 (first entry)
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514643/56.
                              Similarity
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              Query Match
Best Local Simil
Matches 144; C
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                                                                                                                                                                                                                                                                                                                                                                    AAE07901;
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Sequence 1032 AA;

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                                                                                                          GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNBYTIIDCIRNNNSG 120
                                                                                                                                                                                      Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
                                                                                  1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                           ö
Length 1032;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A manganese superoxide dismutase (Mn-SOD) construct.
  100.0%; Score 770; DB 4;
100.0%; Pred. No. 5.4e-68;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hallis B, Silman N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                     WKISLNYNKIIWTLODTAGNNOKL 144
                                                                                                                                                                                                                                                                                            722 WKISLNYNKIIWTLQDTAGNNOKL 745
                                                                                                                                                                                                                                                                                                                                                                                                      AAY93309 standard; protein; 1059 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Geobacillus stearothermophilus.
Clostridium botulinum.
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                                             Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shone CC, Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-376553/32.
                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1998;
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    Query Match
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Sequence 1059 AA;

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61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                 629 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 688
                                                                                                                                                      689 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 748
                                                                   9
                                                                 1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                   Gaps
                                 ö
 Length 1059;
                                 Indels
; Score 770; DB 3;
; Pred. No. 5.5e-68;
0; Mismatches 0;
                                                                                                                                                                                                         WKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                            749 WKISLNYNKIIWTLQDTAGNNQKL 772
                                                                                                                                                                                                                                                                                          2, 2006, 00:38:55
   100.0%;
     Query Match 100.
Best Local Similarity 100.
Matches 144; Conservative
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Job time : 68.993 secs
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- protein search, using sw model OM protein

March Run on:

2, 2006, 00:39:17 ; Search time 12.0278 Seconds (without alignments) 1151.928 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-981-087B-2 770 1 SYTNDKILILYFNKLYKKIK..........LNYNKIIWTLQDTAGNNQKL 144

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database :

PIR 80:\*
1: Pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		عد				
Reguit No.	Score	Match	Length	DB	ID	Description
1	770	100.0	366	. ~	S48110	neurotoxin type F
8	626.5	81.4	369	7	S48109	
m	626.5	81.4	1274	~	140813	neurotoxin type F
4	625	81.2	1268	~	S33411	botulinum neurotox
Ŋ	571.5	74.2	367	~	S48106	neurotoxin type E
9		74.2	1252	~	S21178	botulinum neurotox
7	568.5	73.8	1251	~	JH0256	botulinum neurotox
8	378.5	49.2	1296	-	BTCLAB	bontoxilysin (EC 3
6	377.5	49.0	1296	~	I40645	botulinum neurotox
10	355	46.1	1291	Н	A48940	bontoxilysin (EC 3
11	348	45.2		~	140631	λt
12	319	41.4		~	S39791	neurotoxin - Clost
13	250	32.5		~	A49777	
14	250	32.5		~	S46431	botulinum neurotox
15	249.5	32.4		7	S11455	botulinum neurotox
16	244	31.7		7	S70582	botulinum neurotox
17	206	26.8		Н	BTCLTN	tentoxilysin (EC 3
18	201	26.1		7	A53878	type E neurotoxin
19	125	16.2	-	7	140817	
20	117	15.2		~	B45600	asparagine-rich bl
21	115	14.9	1196	~	JQ1467	toxin, nontoxic co
22	115	14.9		N	S46430	botulinum neurotox
23	114	14.8		~	A47708	progenitor toxin n
24	113	14.7	1193	7	\$68218	botulinum neurotox
25	111.5	14.5		~	C82911	hypothetical prote
26	111.5	14.		7	T38983	probable gtpase ac
27	110	14.3	1193	~	JC4901	nontoxic-nonhemagg
28	105	13.6	430	7	T28318	ORF MSV157 hypothe
29	100.5	13.1	464		MINVUMC	nonstructural prot

hypothetical prote mosquitocidal prot hypothetical brote	arabinogalactan-pr nonstructural prot qene COX1 intron 4	PK4 protein kinase hypothetical prote	hypothetical prote hypothetical prote probable secreted	hypothetical prote hypothetical prote	lipoprotein (impor hypothetical prote toxin-like outer m
C71609 JC6033	T10265 MNVUW1	T28139 S72306	D71615 T18503 A71609	C64432 T28217	G90587 D71612 B64596
01010	4 C1 C	0 0	01010	1010	000
558 613	461 461 467	1123	504 913	537	789 1844 1943
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31	2 E E 2 E E	36	338	4 4 4 2 2	4 4 4 5 4 5

## ALIGNMENTS

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175	110
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neurotoxin type F - Clostridium botulinum (fragment) C;Species: Clostridium botulinum

C; Date: 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S48110 E;Accession: S48110 J; Clin. Microbiol. 31, 2255-2262, 1993 A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48103; MUID:94013372; PMID:8408542 A;Accession: S48110 A;Accession: S48110 A;Accession: S48110 A;Accession: S48110 A;Amolecule type: DNA

A;Residues: 1-366 <CAM>
A;Residues: 1-366 <CAM>
A;Cross-references: UNIPROT:057236; UNIPARC:UPI000016EA7C; EMBL:X70821; NID:g407792; PID
C;Superfamily: tetams toxin
C;Keywords: neurotoxin

ö Gaps ö Query Match 100.0%; Score 770; DB 2; Length 366; Best Local Similarity 100.0%; Pred. No. 3.5e-54; Matches 144; Conservative 0; Mismatches 0; Indels (

214 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 273 9 1 SYTNDKILLLYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF ò В

61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120 274 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVRLNNEYTIIDCIRNNNSG 333 ò

121 WKISLNYNKIIWTLQDTAGNNOKL 144 셤 à

334 WKISLNYNKIIWTLQDTAGNNOKL 357

셤

# RESULT S48109

neurotoxin type F - Clostridium botulinum (fragment) C;Species: Clostridium botulinum

C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 09-Jul-2004

C;Accession: S48109
R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48109

A;Cross-references: UNIPROT:P30996; UNIPARC:UPI000016EA7B; EMBL:X70820; NID:g407790; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 C;Superfamily: tetanus toxin A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-369 <CAM>

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neurotoxin type E - Clostridium botulinum
C;Species: Clostridium botulinum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-367 < CAM>
A,Status: preliminary
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A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Crasd.use: 1-1274 <RES;
A;Crampbell; K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48108
A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 634-1002 <CAM>
A;Cross-references: UNIPARC:UPI000016EA7B; EMBL:X70816; NID:g407788; PIDN:CAAS0147.1; PI
C;Superfamily: tetamus toxin
C;Keywords: neurotoxin
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botulinum neurotoxin type F - Clostridium barati

c/species: Clostridium barati

c/species: Clostridium barati

c/species: Clostridium barati

c/species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

c/shcession: 833411, 831860

R/Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.

FENS Microbiol. Lett. 108, 175-182, 1993

A/Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin
A/Reference number: 833411; MUID:9325228; PMID:8486245
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C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140813; S48108
R;East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, FEMS Microbiol. Lett. 96, 225-230, 1992
A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A;Reference number: 140644
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                                                                                                                                                                                                                                   GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                            214 SYTNDKILIIYFNRLYKKIKDSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQF 273
                                                                                                                                                                                                        GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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                   Length 369;
                                                                  12; Indels
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14; Mismatches 12; Indels
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                   DB 2;
                 Query Match 81.4%; Score 626.5; DB 2
Best Local Similarity 80.3%; Pred. No. 9.6e-43;
Matches 118; Conservative 14; Mismatches 12
                                                                                                                                                                                                                                                                                                                              334 WKISLRTVRDCEIIWTLQDTSGNKENL 360
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neurotoxin type F - Clostridium botulinum
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C)Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C)Accession: 548106
C)Accession: 548106
Cin. Microbiol. 31, 2255-2262, 1993
A)Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A)Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A)Accession: 548106
A)Accession: 548106
A)Status: preliminary; nucleic acid sequence not shown, translation not shown
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Dotulinum neurotoxin type E precursor - Clostridium botulinum

C;Species: Clostridium botulinum

C;Species: Clostridium botulinum

C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 31-Dec-2004

C;Accession: S21178; S48107; JH0257; B35294; A60027; S18111

Exiv. J. Blochem. 204, 657-667, 1992

A;Title: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxir

A;Reference number: S21178; MUID:92174922; PMID:1541280

A;Accession: S21178

A;Molecule type: DNA

A;Residues: 1-1252 <WHE>
A,Molecule type: DNA
A,Residues: 1-1268 <THO>
A,Residues: 1-1268 <THO>
C,SUperfamily: tetamus toxin
C,Superfamily: tetamus toxin
C,Keywords: neurotoxin
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Best Local Similarity 81.1%; Pred. No. 5.2e-42;
Matches 116; Conservative 11; Mismatches 16;
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A, Experimental source: strains ATCC 43181 and ATCC 43755
R, Fujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N. C. Gen. Microbiol. 137, 519-525, 1991
A; Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type B toxi. A; Reference number: S16145; MUID:91237316; PMID:2033376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-229, W, 231-252 <FUJ>
A;Cross-references: UNIPARC:UP1000016EA8F; EMBL:X53180; NID:g40407; PIDN:CAA37321.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Experimental source: strain BL6340; Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release; Comment: The heavy chain mediates the binding of toxin to cell receptors while the lightwarefamily: tetanus toxin
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R;Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T
Bur. J. Biochem. 189, 73-81, 1990
A;Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin
A;Reference number: S09492; MUID:90235864; PMID:2185020
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A;Residues: 1,'Q',3-26,'V',28-1296 <THO>
A;Cross-references:.UNIPARC:UPI000003409D; EMBL:X52066; NID:940381; PIDN:CAA36289.1; PID
Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type ne number: JH0256; MUID:92181428; PMID:1543481
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A;Residues: 1-1296 <BIN>
A;Cross-references: UNIPROT:P10845; UNIPARC:UP10000001386; GB:M30196; NID:g144864; PIDN
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N;Alternate names: botulinum neurotoxin type A
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 31-Mar-1993 Heaquence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000
R;Binz, T; Kurazono, H; Wille, M; Frevert, J; Wernars, K.; Niemann, H.
J:Biol. Chem. 265, 9153-9158, 1990
A;Fitle: The complete sequence of botulinum neurotoxin type A and comparison with A;Reference number: A35294; MUID: 90264400; PMID: 2160960
                                                                                                                                                                                                                                            EMBL: X62088; NID: 940379
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5, 41-44, 1995
                                                                                                                                                                                                                                        UNIPARC: UPI000017670D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.8%; Score 568.5; DB 2; Best Local Similarity 71.0%; Pred. No. 1.6e-37; Matches 103; Conservative 26; Mismatches 15;
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                                                                                                                              A; Status: nucleic acid sequence not shown
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                                                                                              A:Accession: JH0256
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FEBS Lett. 370
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A; Cross-references: UNIPARC:UP1000017670F
A; Cross-references: UNIPARC:UP1000017670F
A; Cross-references: UNIPARC:UP1000017670F
A; Experimental source: strain Beluga
R; Gimenez, J.A.; DasGupta, B.R.
Biochimie 72, 213-217, 1990
A; Title: Borulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the si
A; Reference number: A60027, MUID:90344918; PMID:2116911
A; Reference number: A60027
A; Molecule type: protein
A; Residues: 420-427 <GIM>A; Residues: 420-427 <GIM>A; Residues: 420-427 <GIM>A; Residues: UNIPARC:UP1000176710
A; Residues: UNIPARC:UP1000176710
A; Reperimental source: strain Beluga
A; Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin
C; Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig
C; Keywords: neurotoxin
C; Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig
C; Keywords: neurotoxin
F; 1-422/Product: botulinum neurotoxin type E light chain #status predicted <HCH>
F; 412-426/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Realdues: 616-982 < CAM>
A; Realdues: 616-982 < CAM>
A; Cross-references: UNIPARC:UPI0000BC6F0; EMBL:X70815; NID:g407786; PIDN:CAA50146.1; PI
A; Cross-references: UNIPARC:UPI0000BC6F0; EMBL:X70815; NID:g407786; PIDN:CAA50146.1; PI
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
R; Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
B; Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
A; Title: Sequences of the botulinal neurotoxin & derived from Clostridium botulinum type
A; Reference number: JH0256; MUID:92181428; PMID:1543481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 1-176, R, 178-197, C', 199-339, R', 341-772, I', 774-962, FE', 965-966, R', 968-1
Cross-references: UNIPARC:UPI000016EA7F; EMBL:X62089; NID:940393; PIDN:CAA43999.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain Beluga
R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
N. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other
A;Reference number: A35294; MUID:90264400; PMID:2160960
                       .references: UNIPROT:Q00496; UNIPROT:Q45862; UNIPARC:UP10000010A3; EMBL:X62683;
                                                                                                                                     and specific
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                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
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                                       R.Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
J. Title: Gene probes for identification of the botulinal neurotoxin gene
A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48107
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R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R. Biochem. Biophys. Res. Commun. 183, 107-113, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: nucleic acid sequence not shown
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Dontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum

N;Alternate names: botulinum neurotoxin type B (BONT/B)

C;Species Clostridium botulinum

C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004

C;Accession: A48940; S48105; S21575; A42871; S07155; S08562; S07128; S08573; S08574

E;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.

Appl. Environ. Microbiol. 58, 2345-2354, 1992

A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the ty:
A;Reference number: A48940; MUID:92384550; PMID:1514783
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A, Note: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this public.
R, Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262; 1995
A, Title: Gene probes for identification of the botulinal neurotoxin gene and specific in A, Reference number: $48103; MUID:94013372; PMID:8408542
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A; Residues: 634-994 <CAM>
A; Residues: 634-994 <CAM>
A; Cross-references: UNIPARC: UP1000016EA7A; EMBL: X70817; NID: 9407782; PIDN: CAA50148.1; P
A; Experimental source: proteolytic type B, strain NCTC 7273
R; Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
B; Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
A; Description: Partial amino acid sequence of botulinum neurotoxin type B and comparisis
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A;Residues: 36-217, 'G', 219-224, 'S', 226-246 <SZA>
A;Residues: 36-217, 'G', 219-224, 'S', 226-246 <SZA>
A;Cross-references: UNIPARC:UP1000016EA79; EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PII
R;Kurazono, H.; Mochida, S.; Binz, T.; Eisel, U.; Quanz, M.; Grebenstein, O.; Wernars, J. Biol. Chem. 267, 14721-14729, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1291 <WHE>
A;Cross_references: UNIPROT:P10844; UNIPARC:UP1000016EA76; GB:M81186; NID:9144734; PIDN
                                                                                                                                                                                                                                                                                                                                                     of Clostridium botulinum type
                                                                                                              C;Species: Clostridium botulinum
C;Bate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Bacession: 140645
R;Willems, A.; East, A.K.; Lawson, P.A.; Collins, M.D.
Rs. Microbiol. 144, 547-556, 1993
A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A;Reference number: 140645; MUID:94143603; PMID:8310180
A;Accession: 140645, MUID:94143603; PMID:8310180
A;Accession: 120645; MUID:94143603; PMID:8310180
A;Accession: 120645
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 1-1296 «RES>
A;Cross-references: UNIPROT:Q45894; UNIPARC:UPI000016EA88; EMBL:X73423; NID:g507070; C;Superfamily: tetanus toxin
C;Superfamily: tetanus toxin
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49.0%; Pred. No. 2.8e-22;
:ive 29; Mismatches 43;
                                                                                             botulinum neurotoxin type A - Clostridium botulinum
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KVSLNYGEIIWTLQDNKQNIQRV 997
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A; Status: preliminary
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A;Status: preliminary
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Best Local S
Matches 70
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Arcsestreferences: UNIPARC:UPI0000173655; EMBL:D67030; DDBJ:D50421; NID:g2160224
B;Betley, M.J.; Somers, E.; DasGupta, B.R.
Bacohem. Blophys. Res. Commun. 162, 1388-1395, 1989
A;Title: Characterization of botulinum type A neurocoxin gene: delineation of the N-term A;Reference number: A33401; MUID:89350959; PMID:2669749
A;Accession: A33401
A;Accession: A33401
A;Accession: A33401
A;Accession: A33401
A;Accession: A33401
A;Accession: A33401
A;Coss-references: UNIPARC:UPI000016EA84; GB:M27892; NID:g144880; PIDN:AAA23269.1; PID: KGimence, J.A; DasGupta, B.R.
J; Protein Chem. 12, 351-363, 1993
A;Title: Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and A; Reference number: A53884; MUID:9400342; PMID:8397793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Status: preliminary
A, Molecule type: protein
A, Molecule type: protein
A, Molecule 1867-880,1148-1217, YY, 1219 <GIM>
A, Rossaratiues: 867-880,1148-1217, YY, 1219 <GIM>
A, Cross-references: UNIPARC: UPI00000BBB24; UNIPARC: UPI0000173656
A, Experimental source: strain Hall
A, Experimental source: strain Hall
R, Dasdupta, B.R.; Delieva, M.L.
Biochimie 72, 661-664, 1999
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A;Accession: A60025
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A;Residues: 2-6;445-453,'X',455-457 <DAS1>
A;Residues: USIPARC:UPI0000173657; UNIPARC:UPI0000173658
A;Cross-references: UNIPARC:UPI0000173657; UNIPARC:UPI0000173658
B;DasGupta, B.R.; Folley, J.; Niece, R.
Biochemistry 26, 4162, 1987
A;Title: Partial sequence of the light chain of botulinum neurotoxin type A.
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neurotoxin - Clostridium botulinum
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                                                                                                                            Species: Clostridium botulinum
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Matches 67; Conservative
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A,Molecule type: DNA
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A;Residues: 442-459 <SCH3>
A;Residues: 442-459 <SCH3>
A;Cross-references: UNIPARC:UPI0000173652
R;Cross-references: UNIPARC:UPI0000173652
R;Schiavo, G: Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt A;Reference number: S27125; MUID:93063293; PMID:1331807
A;Contents: annotation
A; Title: Minimal essential domains specifying toxicity of the light chains of tetanus to A; Reference number: A42871; MUID:92340509; PMID:1634516
A, Accession: A42871
A, Accession: A42871
A, Accession: A42871
A, Residue: nucleic acid sequence not shown
A, Residues: 1-313, 'S', 315-451 «KUR>
A, Residues: 1-313, 'S', 315-451 «KUR>
A, Residues: 1-313, 'S', 215-451 «KUR>
A, Residues: 1-313, 'S', 215-451 «KUR>
A, Residues: 1-313, 'S', 215-451 «KUR>
A, Residues: 1-313, 'S', 215-451 «KUR>
A, Residues: 1-313, 'S', 215-451 «KUR>
A, Residues: 1-313, 'S', 215-451 «KUR>
A, Note: sequence extracted from NCBI backbone (NCBIP:109365)
B, R, PasGupta, B.R.; Datta, A.
Biochimie 70, 811-817, 1988
A, Fitle: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with A, Reference number: S07155; MUID:89000987; PMID:3139097
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AjGene: bont/b
AjGene: bont/b
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AjGene: bond in synaptobrevin 2
AjGene: bond in synaptobrevin 2
AjGeneriamily: tetanus toxin
Cjsuperfamily: tetanus toxin
Cjsuperfamily: tetanus toxin
AjGeneriamily: tetanus toxin
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AjGeneriamily: tetanus toxin
AjGeneriamily: tetanus protein; zinc
Fj2441/Product: bontoxilysin B light chain #status experimental chGHT>
Fj242-1291/Product: bontoxilysin B heavy chain #status experimental chVY>
Fj230,224/Binding site: zinc (His) #status predicted
Fj231/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arch. Biochem. Biophys. 238, 544-548, 1985
Afritle: Partial amino acid sequences of botulinum neurotoxins types B
A;Reference number: S07128; MUID:85197963; PMID:3888113
A;Accession: S07128
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larity 47.3%; Pred. No. 1.7e-20;
Conservative 33; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 442-463,'R',465-467 <DA2>
A;Cross-references: UNIPARC:UPI0000173650
R;Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.
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Modecule type: protein
A;Rediques: 2-29, M', 31-45 <DAS>
A;Cross-references: UNIPARC:UPI0000173650
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A;Molecule type: protein
A;Residues: 2-16 <2011.>
A;Cross-references: UNIPARC:UP10000173652
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Best Local Similarity
Matches 69; Conserv
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C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140631; S48103; S48104; S36015
R;Hutson, R.A.; Collins, M.D.; East, A.K.; Thompson, D.B.
Curr. Microbiol. 28, 101-110, 1994
A;Title: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinum A;Reference number: 140631; MUID:94122659; PMID:7764370
A;Accession: 140631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID
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. Clin. Microbiol. 31, 2255-2262, 1993
. Title: Gene probes for identification of the botulinal neurotoxin gene and specific id:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA.
A;Residues: 634-843, T',845, 'N',847-994 «CAM2»
A;Residues: 634-843, T',845, 'N',847-994 «CAM2»
A;Residues: 634-863, T',845, 'N',847-994 «CAM2»
A;Cross-references: UNIPARC:UPI00000B7A6E; EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PI
A;Experimental source: non-proceolytic strain Eklund 2B (Colworth 229)
C;Comment: Botulinum neurotoxin type B in these strains may posses a capable catalytic s
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C.Accession: S39791
R.Campbell, K.; Collins, M.D.; East, A.K.
R.Campbell, K.; Collins, M.D.; East, A.K.
A.Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium A;Reference number: S39791; MUD:94092745; PMID:8268233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Residues: 634-761, E',763-841, M',843, T',845, N',847-994 <CAMI>
"Residues: 634-761, E',763-841, M',843, T', 845, N',847-994 <CAMI>
"Residues: UNIPARC:UPI00000BEAEF; EMBL:X70814; NID:9407778; PIDN:CAAS0145.1; Experimental source: non-proteolytic strain 2129B (Scott)
"Rote: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1.1291 <RES>
Cross-references: UNIPROT:008077; UNIPARC:UPIO0000BDC86; EMBL:X71343; NID:9296148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Keywords: metalloprotein, neurotoxin, transmembrane protein, zinc P;2-441/Product: botulinum neurotoxin type B light chain #status predicted <LGHT> P;42-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HVX> P;230,234/Binding site: zinc (His) #status predicted P;231/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: preliminary, nucleic acid sequence not shown; translation not shown
botulinum neurotoxin type B precursor - Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.2%; Score 348; DB 2; Length 1291;
45.6%; Pred. No. 6.2e-20;
ive 35; Mismatches 39; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number: S48103; MUID:94013372; PMID:8408542
                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated from GB/EMBL/DDBJ
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us-08-981-087b-2.rpr

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A; Molecule type: DNA
A; Residues: 1-1276 <BIN>
A; Cross-references: UNIPROT: P19321; UNIPARC: UPI0000126B83; EMBL: X54254; NID: 940395; PIDNI
C; Superfamily: tetamus toxin
C; Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1291 <HAU>
A;Cross.references: UNIFROT:Q93HT3; UNIPARC:UPI00000B3F60; EMBL:X72793; NID:G516171; PID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain C 468
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Superfamily: tetanus toxin
                                                                                                                                                SYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEEGDVQLNPIFPFDF 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GIYSS--KPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: BoNT/CI protein
Cispecies: Clostridium botulinum phage IC
AyVariety: strain C 468
Cibate: 19-Mar-1997 #sequence revision 06-Jun-1997 #text_change 09-Jul-2004
CiAccession: S46431; 849107
RiHauser, D.; Eklund, M.W.; Boquet, P.; Popoff, M.R.
Mol. Gan. Genet. 243, 631-640, 1994
Airitle: Organization of the botulinum neurotoxin CI gene and its associated a Areference number: S46426; MUID:94301293; PMID:8028579
Aixcession: S46431
Aixtens nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  botulinum neurotoxin type D - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Accession: S1455
R;Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, Nucleic Acids Res. 18, 5556, 1990
A;Title: Nucleotide sequence of the gene encoding Clostridium botulinum neux
A;Reference number: S11455; MUID:91016853; PMID:2216736
A;Reference preliminary; translation not shown
                                                                                              61 GIYSS -- KPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   botulinum neurotoxin C1 - Clostridium botulinum phage 1C (strain C 468) N;Alternate names: BoNT/C1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                       119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
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Best Local Similarity
Matches 52; Conserva
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                    850
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Matches
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S11455
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C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: D. Amar-1994 #sequence revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S11291; A35396; $Z2166; A49777
Nucleic Acids Res. 18, 4924, 1990
A;Title: Nucleotide Sequence of Clostridium botulinum C1 neurotoxin.
A;Reference number: S11291; MUID:90370487; PMID:2204031
A;Reference number: S11291; MUID:90370487; PMID:2204031
A;Residues: Drellminary
A;Molecule type: DNA
A;Residues: Tross-references: UNIPRAC:093HTS; Cupro0016D75D; EMBL:X53751; NID:g14905; PIDN
R;Kimura, K.; Fujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Takeshii, R.
Biochem: Biophys: Res. Commun. 171, 1304-1311, 1990
A;Reference number: A35396; MUID:91024998; PMID:2222445
A;Accession: A35396
A;Residues: Lefoy. R., 671-1291 <TSI>A;Residues: Lefoy. R., 671-1291 <TSI
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A;Residues: R. R. R. R. Pujii, N.; Yokosawa, N.; Oguma, K.
Rumura, K.; Fujii, N.; Yokosawa, N.; Oguma, K.
Rumura, K.; Fujii, N.; Reginium a, A;Residues: Lefoy. R., 771-1291 <TSI
A;Residues: Residues: Lefoy R., 771-1291 TSI
A;Residues: Residues: Lefoy R., 771-1291 TSI
A;Residues: Residues: Lefoy R., 771-1291 TSI
A;Residues: Residues: Residues: Lefoy R.; Pujii, N.; Vokosawa, N.; Oguma, K.
Rumura, K.; Fujii, N.; Rodence Cf the Gene Comparents of the magglutini
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A;Residues: 1-1297 <CAM>
A;Cross-references: UNIPARC:UP10000176706; EMBL:X74162; NID:g441275; PIDN:CAA52275.1;
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                           62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
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                                                                                                                                                                                                              Length 1297;
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                                                                                                                                                                                                                                                                                55; Indels
                                                                                                                                                                                             Query Match
41.4%; Score 319; DB 2;
Best Local Similarity 41.8%; Pred. No. 1.3e-17;
Matches 61; Conservative 26; Mismatches 55
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C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||;|; |:||||| ::::
SGWKVSIKGNRIIWTLIDVNAKSKSI 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGWKISLNYNKIIWTLODTAGNNOKL 144
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A;Molecule type: DNA
A;Residues: 1-607 <TS3>
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G.; Kozaki, S.; Kriegls

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846 SYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVGDNVQLNTIYTNDF 905
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<sup>121</sup> WKISLNYNKIIWTLODTAGNNOK 143 ||::||||||| 962 WKLCIRNGNIEWILQDV---NRK 981

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g ò Search completed: March 2, 2006, 00:47:41 Job time : 13.0278 secs

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RESULT 2
Q57236 CLOBO
ID Q57236_CLOBO PRELIMINARY;
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SEQUENCE
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(c) 1993 - 2006 Biocceleration Ltd.
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BXF_CLÖBO
Q9ZAJ5_CLOBO
Q45851_9CLOT
Q45861_CLOBO
Q54A79_CLOBO
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Q9FAR6_CLOBU
Q9K395_CLOBU
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Q57236_CLOBO
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Maximum Match 100%
Listing first 45 summaries
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2: uniprot_trembl:*
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length: 2000000000
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999tg7 clostridium
P1931 clostridium
Q91br1 clostridium
Q95967 clostridium
Q91013 clostridium
Q93027 clostridium
Q9511 clostridium
Q9511 clostridium
Q9531 clostridium
Q9539 clostridium
Q9539 clostridium
Q9539 clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWYRIPKYFNKVNLNNEYTIIDCIRNNNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=type F;
MEDLINE=94013372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
Campbell K.D., collins M.D., East A.K.;
specific identification of the botulinal neurotoxin gene specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium. WCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Campbell K.D.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 AA; 43136 MW; 45A132B235D7E640 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) sequence in neurotoxin type F (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 770; DB 2;
Pred. No. 4.8e-55;
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                                                                                                                             09R5H1_CLOBO
045888_CLOBO
033871_CLOBO
09ZAJ9_CLOBO
P71117_CLOBO
             09QTG7_CBDP
BXD_CLOBO
Q9LBR1_CLOBO
Q45967_CLOBO
                                                                                                                                                                                                                                                                    ALIGNMENTS
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HSSP; P04958; 1A8D.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                CLOTE
                                                                                                                                                                                                                 006018 CLOBO
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Conservative 0
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                                                                                                                                                                                                                                                                                                                                                    Q79AH9_CLOBO PRELIMINARY;
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Clostridium botulinum.
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Curr. Microbiol. 29:69-77(1994)
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                                                                                                     OF 1-64.
                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION OF SUBSTRATE.
                                                                                                   NUCLEOTIDE SEQUENCE
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                                                          BONT/F (Neurotoxin type F).
Name-bont/f; Synonyms=bonT/F;
Clostridium boculinum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type P precursor (EC 3.4.24.69) (BoNT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain;
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                                                                                                                                                                                                                                            Elmore M.J., Bodsworth N.J., Whelan S.M., Minton N.P.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X81714; CAR57358.1; -; Genomic_DNA.
EMBL; 153496; AAA23210.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1278 AA; 147073 MW; AIBE1318431D6918 CRC64;
                                                                                                                                                                                         Hutson R.A., Collins M.D.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    HSSP, 045894; IEIH.

MEROPS; M27.002; -...

GO; 000:0016021; C:integral to membrane; IEA.

GO; GO:0009405; P:metallopeptidase activity; IEA.

GO; GO:0009405; P:metallopeptidase activity; IEA.

GO; GO:0009405; P:pethogenesis; IEA.

R InterPro; IPR0011591; Botulinum.

R InterPro; IPR0010395; Peptidase_M27.

R InterPro; IPR006025; Pept M_Zn_BS.

R Pfam; PF01742; Peptidase_M27.

R PROSITYS; PR00760; BOWTOXITYSIN.

R PROSITYS; PR001563; Botulinum; 1.
            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 770; DB 2;
100.0%; Pred. No. 1.8e-54;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botulinum neurotoxin F heavy chain]
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STRAIN=Type F / ATCC 23387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                             STRAIN-NCTC 10281;
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                                                                                                                    Clostridium.
NCBI_TaxID=1491;
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RESULT 3

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RK MEDLINE-94230352; PubMed-8175689;

RA MEDLINE-94230352; PubMed-8175689;

RA Yamasaki S., Baumeister A., Birz T., Blasi J., Link E., Cornille F.,

RA Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;

ROQUES B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;

ROQUES B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;

RT "Cleavage of members of the synaptobrevin, VAMP family by types D and F

Broulinal neurotoxins and tetanus toxin.",

L. FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter

CC and moves by retrograde transport up the axon into the spinal cord

where it can move between postsynaptic and presynaptic neurons. It

inhibits neurotransmitter release by acting as a zinc

endopeptidase that catalyzes the hydrolysis of the 58-Gln-|-Lys-59

condopeptidase that catalyzes the hydrolysis of the 58-Gln-|-Lys-59

condopeptidase that catalyzes the hydrolysis of proteins of the

neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No

detected action on small molecule substrates.

condopeptidase action on small molecule substrates.

condoped action on small molecule substrates.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=TYPE F / Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
Rast A.K., Collins M.D.;
"Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteolytic Clostridium botulinum type F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE OF 634-1002.
MEDLINE=94013372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
MEDLINE-93012902; PubMed=11998040; DOI=10.1016/0378-1097(92)90408-G; East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A., Thompson D.E.;
                                                                                                                                                                             'Sequence of the gene encoding type F neurotoxin of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M92906; AAA23263.1; -; Genomic_DNA.

EMBL; S73676; AAC60475.1; -; Genomic_DNA.

EMBL; X70820; CAA50151.1; -; Genomic_DNA.

EMBL; X70816; CAA50147.1; -; Genomic_DNA.

PIR; 140813; 140813.
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InterPro; IPR001995; Peptidase M27.
InterPro; IPR012928; Toxin recpt bd_N.
InterPro; IPR012920; Toxin trans.
Pfam; PF01742; Peptidase M27; 1.
Pfam; PF07952; Toxin R bind N; 1.
Pfam; PF07952; Toxin trans; 1.
PRINTS; PR00760; BONTOXILYSIN.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
FROSITE; PS001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
FROFIDESE; Metal-binding; Metalloprotease; Neurotoxin; Protease;
Toxin; Transmenbrane; Zinc.
                                                                            Botulinum neurotoxin F light chain.
Botulinum neurotoxin F heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heavy
                                                                                                                                                                                                            DB 1; Length 1274;
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                                                                                                                                                                                                         81.4%; Score 626.5; DB 1; Length 80.3%; Pred. No. 1.1e-42; ive 14; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNKNOWN 1.
D0F748976EBC222C CRC64;
                                                                                                                                                                 chains) (Probable).
1274 AA; 146710 MW; 5B99756A7438B921 CRC64;
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Santos-Buelga J.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Y13631; CAA73972.1; -; Genomic_DNA.
HSSP; Q45894; IEIH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; CO: 0016021; C:integral to membrane; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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Last annotation update)
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InterPro; IPRO00395; Peptidase M27.
InterPro; IPR006025; Pept M Zn BS.
Pfam; PP01742; Peptidase M27; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curr. Microbiol. 37:312-318(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSZAJS CLOBO PRELIMINARY;
                                                                                                                                                                                                         Query Match
Best Local Similarity 80.3
Matches 118; Conservative
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STRAIN-CDC 3281;
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ACT SITE
METAL
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                                                                                                                                                                                             61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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PEMS Microbiol. Lett. 108:175-182(1993).
EMBL; X68262; CAA48329.1; -; Genomic_DNA.
PIR; S33411; S33411.
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BEDLINE-3152228; PubMed=8486245; DOI=10.1016/0378-1097(93)90581-L;
Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.,
Richardson P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Length 1280;
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                                                Indels
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GO: GO: 0008237; F:metallopeptidase activity; IEA.
GO: GO: 0008237; F:metallopeptidase activity; IEA.
GO: GO: 0008508; F:pathogenesis; IEA.
InterPro: IPR011591; Botulinum.
InterPro: IPR011591; Botulinum.
InterPro: IPR001035; Peptidase M27.
InterPro: IPR006025; Peptidase M27.
InterPro: IPR006025; Peptidase M27.
IPRINTS; PR00760; BONTOXILYSIN.
PROSITE; PR001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
  81.2%; Score 625.5; DB 2;
80.3%; Pred. No. 1.3e-42;
                              Pred. No. 1.3e
13; Mismatches
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Matches 116; Conservative
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                              Best Local Similarity 80.39
Matches 118; Conservative
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STRAIN-BL6340
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TBukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa T., Nakamura S., Karasawa T., Kozaki S., Sarasawa T., Kozaki S., Karasawa T., Kozaki S., Sequence of the botulinum neurotoxin type E.";
Sequence of the botulinum neurotoxin type E.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
                                                                                                                                                                                                                  Clostridium botulinum.
Bacteria, Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
Clostridium.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AA; 42902 MW; 346A610C2FF70262 CRC64;
                                                                                                                   Last sequence update)
Last annotation update)
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13-5EP-2005 (TrEMBLrel. 31, Last sequence update)
13-5EP-2005 (TrEMBLrel. 31, Last annotation update)
Botulinum neurotoxin type E.
Name=DonL/E,
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                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequenc
01-OCT-2003 (TrEMBLrel. 25, Last annotat
Botulinum neurotoxin type E (Fragment).
Name=BONT/E;
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                                   PRT;
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GO; GO:0009405; P:pathogenesis; IEA.
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              Q45861_CLOBO PRELIMINARY;
Q45861;
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Q54A79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-type E;
Campbell K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104;
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"Neurotoxin type E from Clostridium botulinum and C. butyricum;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";
FASEB J. 2.41750-41750(1988).
-!- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter
release. It binds to peripheral neuronal synapses, is internalized
and moves by retrograde transport up the axon into the spinal cord
where it can move between postsynaptic and presynaptic neurons. It
inhibits neurotransmitter release by acting as a zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endopeptidase.

ANALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

CORACTOR: Binds 1 zinc ion per subunit (By similarity).

SUBUNIT: Disulfide-linked heterodomer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
                                                                                                                                                1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loning of a DNA fragment encoding the 5'-terminus of the botulinum pe E toxin gene from Clostridium butyricum strain BL6340."; Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.; "Cloning of a DNA fragment encoding the 5'-terminus of the botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 43181, and ATCC 43755;
MEDIATR=29181428; PubMed=154481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755) ";
Biochem. Biophys. Res. Commun. 183:107-113(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last amotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
(Bontoxilyain E) [Contains: Botulinum neurotoxin E light chain;
Botulinum neurotoxin E heavy chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                    Length 1252;
                                                                                                           Indels
Neurotoxin.
SEOUENCE 1252 AA; 143637 MW; 76401D4D2E95D7A2 CRC64;
                                                               74.2%; Score 571.5; DB 2; 71.7%; Pred. No. 3.3e-38; ive 25; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1250 AA.
                                                                                                                                                                                                                                                                                                                     GWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                       MEDLINE=91237316; PubMed=2033376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE OF 1-251.
                                                                                                       Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium butyricum.
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                                                                                   Local Similarity
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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF
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Wang X., Maegawa T., Karagawa T., Kozaki S., Tsukamoto K., Gyobu Y.,
Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
Genetic analysis of type B botulinum toxin-producing Clostridium
butyricum strains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium butyricum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.8%; Score 568.5; DB 2; Length 1252; 71.0%; Pred. No. 5.9e-38; ive 26; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41B633BB744D3B41 CRC64;
              Teukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Teukamoto K., Karasawa T., Kozaki S.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; ABO88207; BAC05434.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR010591; Boculinum.
InterPro; IPR000395; Peptidase_M27.
InterPro; IPR000395; Peptidase_M27.
PEAM; PF01742; Peptidase_M27; I.
PRINTS; PR00760; BONTOXILIVSIN.
ProDom; PD001963; Botulinum; 1.
                                                                                                                                                                                  CO. GO:0016021, C:integral to membrane; IEA.
GO; GO:0008371; F:metallopeptidase activity; IEA.
GO; GO:0009405; F:metallopeptidase activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001591; Botulinum.
InterPro; IPR001595; Peptidase M27.
InterPro; IPR00055; Peptidase M27.
Pfam; PP01742; Peptidase M27; I.
PRINTS; PR00760; BONTOXILYSIN.
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Last annotation update)
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EMBL, AB039264; BAB12249.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1252 AA; 143510 MW; 41B633BB74
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MEDLINE=20509829; PubMed=11055954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.0%;
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Q9FAR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.8%;
Best Local Similarity 71.0%;
Matches 103; Conservative
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                                                                                                                                                             SMR; O8KZM3;
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Q9FAR6_CLOBU
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                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROFESE; 1.
PROSITE; PS00142; ZINC_PROFESE; 1.
Noirect protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
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                          MISCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 211 Zinc (catalytic) (By similarity).
215 215 Zinc (catalytic) (By similarity).
411 425 Interchain (between light and heavy catalys).
229 229 K -> M (in Ref. 2).
1250 AA; 143266 MW; 8171B5B2C2312857 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
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Botulinum neurotoxin E heavy chain.
By similarity.
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                                                                                                                                                                                                                                                                                                        EMBL; X62088; CAA43998.1; -; Genomic_DNA.
EMBL; X53180; CAA37321.1; -; Genomic_DNA.
PIR; JH0256; JH0256.
PIR; P36994; IEIH.
SWR; P30995; 1-411.
MEROPS; M27.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AnterPro; IPR006025; Pept M Zm. BS.

R InterPro; IPR000395; Pept M Zm. BS.

R InterPro; IPR000395; Peptidase M2.

R InterPro; IPR012928; Toxin_recpt bd.

Pfam; PF01742; Peptidase M27; 1.

Pfam; PF07952; Toxin_R bind_N; IPRM, PF07952; Toxin_trans.

Pfam; PR07952; Toxin_R bind_N; IPRM, PF07952; Toxin_trans.
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QBKZM3;
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Clostridium butyricum.
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STRAINELCL 095, LCL 155, KZ 1899, KZ 1897, KZ 1898, KZ 1886, KZ 1887, KZ 1899, KZ 1890, KZ 1891, KZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, WZ 1891, W
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Clostridium.
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                                                                                DB 2; Length 1255;
PS00142; ZINC PROTEASE; UNKNOWN 1.
1255 AA; 143917 MW; 1B557B9DBSCD8E4D CRC64;
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2021F4E427070296 CRC64;
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GO; GO:0009405; F:peptidase activity; IEA.
GO; GO:000508; F:proteolysis and peptidolysis; IEA.
GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
InterPro; IPR01151; Botulinum.
InterPro; IPR010519; Pept M Zn BS.
InterPro; IPR010395; Pept M Zn BS.
InterPro; IPR012928; Toxin reapt bd N.
InterPro; IPR012928; Toxin reapt bd N.
InterPro; IPR012500; Toxin reapt bf M.; PR01742; Peptidase MZ7; 1.
Pfam; PR01742; Peptidase MZ7; 1.
Pfam; PR01953; Toxin R bind N; 1.
Pfam; PR01953; Toxin R bind N; 1.
Probon; PR01953; Botulinum; 1.
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                                                                        13.8%; Score 568.5; DB 2 ilarity 71.0%; Pred. No. 5.9e-38; Conservative 26; Mismatches 15
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EMBL, AB037706; BAB0314.1; -; Genomic_DNA.
EMBL, AB037712; BAB03518.1; -; Genomic_DNA.
EMBL, AB037712; BAB03520.1; -; Genomic_DNA.
EMBL, AB037713; BAB03521.1; -; Genomic_DNA.
EMBL, AB037709; BAB03519.1; -; Genomic_DNA.
EMBL, AB037709; BAB03517.1; -; Genomic_DNA.
EMBL, AB037709; BAB03515.1; -; Genomic_DNA.
EMBL, AB037709; BAB03515.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                       952 GWKVSLNHNEIIWTLQDNSGINQKL 976
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Q9K395;
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PROSITE; 1
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                                                                                                     829 SYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGEIFIYPTNKNQF
                                                                                                                                                                                  889 TIFNSKPSEVNISQNDYIIXDNKYKNFSISFWVRIPNYDNKIVNINNEYTIINCMRDNNS
                                                                               1 SYTNDKILLILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYLYSTNRNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92174922; PubMed=1541280; Whelan S. Limbon N.P.; Whelan S.M.; Elmore M.J.; Bodsworth N.J.; Atkinson T.; Minton N.P.; "The complete amine acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90264400; bubMed=2160960;

Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;

"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins";
J. Biol. Chem. 265:9153-9158(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
Sequences of the botulinal neurotoxin B derived from Clostridium
botulinum type E (strain Beluga) and Clostridium butyricum (strains
ATCC 43181 and ATCC 43755).",
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                          000496; Q45862;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurocoxin type B precursor (EC 3.4.24.69) (BONT/E)
(Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain;
Botulinum neurocoxin E heavy chain].
                                         1,
    Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.; "Partial amino acid sequences of botulinum neurotoxins types
                                         Indels
73.3%; Score 564.5; DB 2; 69.7%; Pred. No. 1.3e-37; ive 29; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 183:107-113(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arch. Biochem. Biophys. 238:544-548(1985).
                                                                                                                                                                                                                                         GWKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                             949 GWKVSLNHNEIIWTLODNARINOKL 973
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MEDLINE=92181428; PubMed=1543481;
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MEDLINE=94013372; Pubmed=8408542;
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Query Match
Best Local Similarity 69.7%
Matches 101; Conservative
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J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Chease It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 180-Arg-|-11e-

J. Manaparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

J. SUBNIT: Disulfide-linked heterodimer of a light chain (H). The light chain has the pharmacological activity, formation and toxin binding, respectively.

J. SUBCLIULAR LOCATION: Secreted.

J. MINCELLULAR LOCATION: Secreted.

J. MINCELLULAR LOCATION: Secreted.

J. MINCELLULAR LOCATION: Types A, B, C1, D, E, P, and G.

J. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                neurotoxin gene and
                                                                 IDENTIFICATION OF SUBSTRATE.
MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Bottenati F., Wilson M.C., Montecucco C.; COH-terminal peptide bonds ", FEBS Lett. 335:99-103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-structure; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc. 0 101T MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Botulinum neurotoxin E light chain.
Botulinum neurotoxin E heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heavy
Campbell K.D., Colling M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxis specific identification of neurotoxin types B, E, and F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X62089; CAA43999.1; -; Genomic_DNA.
EMBL; X62683; CAA44558.1; -; Genomic_DNA.
EMBL; X70815; CAA50146.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR011591; Botulinum.
InterPro; IPR0105025; Pept M Zn BS.
InterPro; IPR0005025; PeptIdase_M27.
InterPro; IPR0102928; Toxin_recpt_bd_N.
InterPro; IPR012500; Toxin_trans.
Pfam; PP01742; Peptidase_M27; 1.
Pfam; PP07953; Toxin_R bind_N; 1.
Pfam; PP07952; Toxin_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S08575; S08575.
PIR; S21178; S21178.
PDB; 1T3A; X-ray; A/B=1-421.
PDB; 1T3C; X-ray; A/B=1-421.
                                                                                                                                                                                         IDENTIFICATION OF SUBSTRATE.
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212
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DISULPID
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MBDLNES-97016817; PubMed=8863443;
Bast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
Bast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
Companization and phylogenetic interrelationships of genes encoding
components of the botulinum toxin complex in proteolytic Clostridium
botulinum types A, B, and F: evidence of chimeric sequences in the
gene encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Type A / 62A;
MEDLINE=90264400; PubMed=2160960;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
With complete sequence of bottlinum neurotoxin type A and comparison
with other clostridial neurotoxins.";
J. Biol. Chem. 265:9153-9158(1990).
                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson D.E., Brehm J.K., Oultram J.D., Swinfield T.-J., Shone C.C. Atkinson T., Melling J., Minton N.P.; "The complete amino acid sequence of the Clostridium botulinum type neurotoxin, deduced by nucleotide sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P10845; P01561; P18639; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BONT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                 Length 1250;
                   176 R -> G (in Ref. 2).
197 C.-> S (in Ref. 2 and 3).
339 R -> A (in Ref. 2).
772 I -> L (in Ref. 2 and 6).
963 FE -> LQ (in Ref. 2 and 6).
966 R -> A (in Ref. 2 and 6).
1194 N -> NN (in Ref. 2 and 6).
143713 MW; D9FCEZ6DDA041EB4 CRC64;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                            D9FCE26DDA041EB4 CRC64;
                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                           DB 1;
(Probable).
                                                                                                                                                                                                                                                              ; Score 559.5; DB 1
; Pred. No. 3.2e-37;
26; Mismatches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:||:||:||| :| | |||| GWKVSLNHNEIIWTFEDNRGINOKL 972
chains)
R -> G (:
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MEDLINE=90235864; PubMed=2185020;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=botA; Synonyms=atx, bna;
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NUCLEOTIDE SEQUENCE OF 1-34.
STRAIN=TYPE A / Hall;
                                                                                                                                                                                                                                                                 72.78;
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1250 AA;
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MEDLINE=85285016; PubMed=3896784; Shone C.C., Hambleton P., Melling J.; Shone C.C., Hambleton P., Melling J.; "Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity."; Eur. J. Blochem. 151:75-82(1985).
                                                                                                                                                                                                                                                                                                        Dasgupta B.R., Foley J., Niece R., Hartial sequence of the light chain of botulinum neurotoxin type A.", Biochemistry 26:4162-4162(1987).
                                                                                                                        Fujita R., Fujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K., "Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins.";
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Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C., Jahn R., Niemann H., Miemann H., Riemann H., Wiemann B., Suedhof T.C., "Protecolysis of SNAP-25 by types E and A botulinal neurotoxins."; J. Biol. Chem. 269:1617-1620(1994).
                                                                                            STRAIN=TYPE A / NIH;
MEDLINE=96096783; PubMed=8521962; DOI=10.1016/0014-5793(95)01241-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION OF SUBSTRATE.

MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schlavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Benfenati F., Wilson M.C., Montecucco C.; Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOM-terminal peptide bonds.";
           Betley M.J., Somers E., Dasgupta B.R.; "Characterization of botulinum type A neurotoxin gene: delineation
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91120847; PubMed=2126206; DOI=10.1016/0300-9084(90)90048-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 448-474 AND 872-895.
MEDLINE-898024662; PubMed=3178218;
Sathymoorthy V., Dasgupta B.R., Foley J., Niece R.L.;
"Betulinum neurotoxin type A: Cleavage of the heavy chain into two halves and their partial sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gimenez J.A., DasGupta B.R.; Botulinum type A neurotoxin digested with pepsin yields 132, 97, 45, 45, and 18 M fragments 1. Yerotein Chem. 12:351-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                             Dasgupta B.R., Dekleva M.L.; "Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site."; Biochimie 72:661-664(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
                                                                                                                                                                                                                        Schmidt J.J., Sartymoorthy V., Dasgupta B.R.; "Partial amino acid sequence of the heavy and light chains of botulinum neurotoxin type A.";
                                      the N-terminal encoding region.";
Biochem. Biophys. Res. Commun. 162:1388-1395(1989)
                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 119:900-904(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch. Biochem. Biophys. 266:142-151(1988)
                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEQUENCE OF 1-5 AND 444-456.
MEDLINE=89350959; PubMed=2669749;
                                                                                                                                                                                              PROTEIN SEQUENCE OF 1-16.
MEDLINE=84178501; PubMed=6370252;
                                                                                                                                                                                                                                                       neurotoxin type A.";
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                                                                                 NUCLEOTIDE SEQUENCE OF 1-18.
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                                                                                                                                                                  Lett. 376:41-44 (1995)
                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 1-46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8397793;
                                                                                                                                                   components of
FEBS Lett. 376
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-i- FUNCTION: Inhibite acceptancy operipheral neuronal presynaptic
membrane, is then internalized by receptor-mediated endocytosis.
The C-terminus of the heavy chain (H) is responsible for the
adherence of the toxin to the cell surface while the N-terminus
mediates transport of the light chain from the endocytic vesicle
to the cytosol. After translocation, the light chain (L)
hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking
neurotransmitter release. Inhibition of acetylcholine release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- PHARMACEUTICAL: Available under the name BOTOX (Allergan) for the treatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.

-i- MSCELLANGROUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.

-i- SIMILARITY: Belongs to the peptidase M27 family.

-i- DATABASE: MAME-BOTOX product information Web site;
                                                                                                                                                                                                 MEDLINE=98455071; PubMed=9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

COPACTOR: Binds 1 zinc ion per subunit.

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WWW="http://www.botox.com/site/".
DATABASE: NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              results in flaccid paralysis, with frequent heart or respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WWW="http://www.expasy.org/spotlight/back_issues/sptlt019.shtml"
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"Site-directed mutagenesis identifies active-site residues of the light chain of botulinum neurotoxin type a."; Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
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Botulinum neurotoxin A heavy-chain.
Potential.
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PROSITE; PS00142; ZINC_PROTEASE; I.
3D-etructure; Direct protein sequencing; Hydrolase; Metal-bind Metalloprotesse; Neurotoxin; Pharmaceutical; Protease; Toxin; Transmembrane; Zinc.
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EMBL; M30196; AAA23262.1; -; Genomic_DNA.
EMBL; X92973; CAA63551.1; -; Genomic_DNA.
EMBL; D67030; BAA11051.1; -; Genomic_DNA.
EMBL; M27892; AAA23269.1; -; Genomic_DNA.
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR000395; Pept M Zn BS.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012908; Toxin recpt bd N.
InterPro; IPR012500; Toxin trans.
Pfam; PF01742; Peptidase M77; 1.
Pfam; PF07953; Toxin E bind N; 1.
Pfam; PF07953; Toxin Erans; 1.
PRINTS; PR00760; BONTOXILYSIN.
                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                     toxicity.";
Nat. Struct. Biol. 5:898-902(1998)
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PDB; 3BTA; X-ray; A=1-1295.
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STRAIN=Allergan-Hall A;
MEDLINE=22919384; PubMed=14557061; DOI=10.1016/S0378-1119(03)00792-3;
Zhang L., Lin M.J., Li S., Aoki K.R.;
"Complete DNA sequences of the botulinum neurotoxin complex of
Clostridium botulinum type A-Hall (Allergan) strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dineen S.S., Bradshaw M., Johnson E.A.; "Neurotoxin gene clusters in Clostridium botulinum type A strains: sequence comparison and evolutionary implications."; Curr. Microbiol. 46:345-352(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Hall A-hyper;
MEDLINE=22617869; PubMed=12732962; DOI=10.1007/800284-002-3851-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                   E->A: Drastic decrease in enzymatic
                                                                                                                              Interchain (between light and heavy
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                                                                                                                                                                                                                                                                                 Score 378.5; DB 1; Length 1295; Pred. No. 2.3e-22;
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Last annotation update)
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                                                                         (catalytic)
                                                    (catalytic)
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EMBL; AF488749; AAQ06331.1; -; Genomic_DNA.
Potential.
                                                                                                                                                      chains).
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                                                    Zinc
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Best Local Similarity
Matches 69; Conserv
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Best Local
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MUTAGEN
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This Swiss-Prot entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln. |-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97016817; PubMed=8863443;

MEDLINE=97016817; PubMed=8863443;

Rast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

Rast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

Components of the botulinum toxin complex in proteolytic Clostridium botulinum types A. B. and P. evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";

Jin. J. Syst. Bacteriol. 46:1105-1112(1996).

--- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       results in flaccid paralysis, with frequent heart or respiratory failure (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Type A / Kyoto-F;
MEDLINE=94143603; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. detected action on small molecule substrates. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 failure (By Similarity). CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy chain (H) (By similarity).
SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Willems A., East A.K., Lawson P.A., Collins M.D.,
"Sequence of the gene coding for the neurotoxin of Clostridium
byldinum type A sasociated with infant botulism: comparison with
other clostridial neurotoxins.",
Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
(Boncoxilyain A) (BOTA) (Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain].
                                                                                                                                                                                                                                                                                                                                      Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                            PRT; 1295 AA
122 KISLNYNKIIWTLODTAGNNOKL 144
                        Name=botA; Synonyms=atx, bna;
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                                                                                                                                              STANDARD;
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                                                                                                                                            BXA2 CLOBO (045894; P77780;
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                                                                                                  RESULT 15
BXA2 CLOBO
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EMBL; X73423; CAA51824.1; -; Genomic\_DNA. EMBL; X87974; CAA61234.1; -; Genomic\_DNA. PIR; 140645; 140645. PDB; 181H; X-ray; A/C=9-249; B/D=250-415.

removed

MEROPS; M27.002; -. InterPro; IPR011591; Botulinum.

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2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKPIDISGYGSNISINGDVYIYSTNRNQFG 61
R InterPro; IPR006025; Pept_M_Zn_BS.
R InterPro; IPR0102928; Toxin_recpt_bd_N.
InterPro; IPR012928; Toxin_recpt_bd_N.
InterPro; IPR012928; Toxin_recpt_bd_N.
R InterPro; IPR012500; Toxin_rena.
R Pfam; PF07953; Toxin_trans.
R Pfam; PF07953; Toxin_trans.
R Pfam; PF07953; Toxin_trans.
R Pfam; PF07953; Toxin_trans.
R PRINTS; PR00160; BONTOXILYSIN.
R PROSTTE; PR00142; ZINC_PR0TEASE; FALSE_NEG.
N 3D-structure; Hydrolane; Metal-binding; Metalloprotease; Neurotoxin;
N Protease; Toxin; Transmembrane; Zinc.
R NTI_MET 0 By similarity.
CHAIN 448 1295 Botulinum neurotoxin A heavy-chain.
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625 675 Potential.
223 222 Zinc (catalytic) (By similarity).
226 226 Zinc (catalytic) (By similarity).
429 453 Interchain (between light and heavy channs) (By similarity).
1234 1279 By similarity.
1295 AA; 149280 MW; 5DA04Al3D98D6372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
49.0%; Score 377.5; DB 1; Length 1295;
Best Local Similarity 49.0%; Pred. No. 2.8e-22;
Matches 70; Conservative 29; Mismatches 43; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 KISLNYNKIIWTLQDTAGNNQKL 144
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Search completed: March 2, 2006, 00:46:24 Job time : 74.8376 secs

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GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 2, 2006, 00:46:47; Search time 17.7077 Seconds (without alignments) 672.325 Million cell updates/sec

Title: US-08-981-087B-2
Sequence: 1 SYTNDKILILYFNKLYKKIK.........LNYNKIIWTLQDTAGNNQKL 144

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/laa/5\_COMB.pep:\*

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 ase : Issued\_Patents\_AA:\*

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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/PCCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	QI	Description
1	378.5	49.2	1296	-	US-08-480-604A-28	28,
7	378.5	49.2	1296	н	US-08-405-496A-28	28,
m	378.5	49.2	1296	7	US-08-915-136-28	28,
4	378.5	49.2	1296	~	US-09-084-517-28	28,
'n	377.5	49.0	848	7	US-10-360-101-219	219,
y	371.5	48.2	438	Н	US-08-480-604A-23	23,
7	371.5	48.2	438	ч	US-08-405-496A-23	23,
80	371.5	48.2	438	7	US-08-915-136-23	23,
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15	355	46.1	1290	7	US-10-360-101-220	Sequence 220, App
16	277.5	36.0	382	N	US-09-288-326A-9	6
17.	277.5	36.0	382	~	US-09-548-409B-9	ď
18	209	27.1	452	٦	US-07-618-312A-2	~
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20	206	26.8		-	US-07-618-312A-4	4,
21	206	26.8		Н	US-08-280-228-4	4
22	206	26.8		Н	US-08-668-381A-5	Z,
23	206	26.8		N	US-08-913-880C-17	17
24	206	26.8	828	~	US-08-913-880C-16	Sequence 16, Appl
25	206	26.8		~	US-08-913-880C-15	15,
26	206	26.8		7	US-08-913-880C-14	14,
27	. 206	26.8	865	7	US-08-913-880C-13	Sequence 13, Appl

Sequence 12, Appl Sequence 11, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 21, Appl Sequence 21, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 2933, Appl Sequence 2933, Appl Sequence 2933, Appl Sequence 2933, Appl Sequence 30, Appl	Sequence 12, Appl
US-08-913-880C-12 US-08-913-880C-10 US-08-913-880C-10 US-08-913-880C-10 US-08-110-786A-8 US-08-110-786A-8 US-09-150-741-2 US-09-150-741-2 US-09-150-741-2 US-09-150-741-2 US-09-180-422B-27 US-09-180-422B-27 US-09-180-06C-1 US-09-134-001C-2993 US-09-134-001C-2993 US-08-836-687B-30 US-09-662-254B-30	US-08-495-484-12
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# ALIGNMENTS

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US-08-480-604A-28

US-08-480-604A-28

Sequence 29, Application US/08480604A

Patent No. 5785139

GENERAL INFORMATION:

APPLICANT: KINK, JOHN A.

APPLICANT: THALLEY, BRUCE S.

APPLICANT: FRCA, JOSEPH N.

APPLICANT: FRCA, JOSEPH N.

APPLICANT: FRCA, JOSEPH N.

APPLICANT: FRCA, JOSEPH N.

APPLICANT: FRCA, JOSEPH N.

APPLICANT: SAPPRORD, DOUGLAS C.

TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 MONTCOMENT STREET, SUITE 2200

CITY: SAN FRANCISCO

CONTRY: UNITED STATES OF AMERICA

COMPTRY: UNITED STATES OF AMERICA

COMPUTER TRADABLE FORM:

MURBIUM TYPE: PLOPEY disk

COMPUTER: TRADABLE FORM:

MURBIUM TYPE: PLOPEY MISK

COMPUTER: TRADABLE FORM:

MURBIUM TYPE: PLOPEY WISK

COMPUTER: TAPPLICATION DATA:

APPLICATION WUMBER: US 08/422,711

FILING DATE: 14-APR-1995

RIUNG APPLICATION NUMBER: US 08/161,907

FILING DATE: 16-APR-1992

FRIUNG APPLICATION DATA:

APPLICATION WUMBER: US 08/161,907

FRIUNG DATE: 25-CCT-1994

FILING DATE: 25-CCT-1994

FILING DATE: 25-CCT-1994

FILING DATE: 25-CCT-1994

FILING DATE: 25-CCT-1994

FILING DATE: 31-CCT-1994

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS.
                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-405-496A-28
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                                                                                                                                                                                                                                                                                                                                                                                          916 LEWLESSKIEVILKMALVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW 974
                                                                                                                                                                                                                                                                                              2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                 Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08405496A

Patent No. 5919665

GENERAL INFORMATION:

APPLICANT: WILLIAMS, JAMES A.

TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM

TITLE OF SQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA
                                                                                                                                                                                                                                                                   42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.2%; Score 378.5; DB 1; 48.3%; Pred. No. 5.8e-31;
                                                                                                                                                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-MAR-1995
CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 25-OCT-1994
FILING DATE: 02-DC-1993
APPLICATION DATA: 08/161,907
FILING DATE: 02-DEC-1993
FILING DATE: 04-DEC-1993
FILING DATE: 04-DEC-1992
FILING DATE: 04-DEC-1992
FILING DATE: 04-DEC-1993
FILING DATE: 04-DEC-1989
ATPORNEY FABRICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY FABRICATION NUMBER: 40,027
REGISTRATION NUMBER: 40,027
REGISTRATION NUMBER: 09HD-01308
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TELEFAX: (415) 397-8338
REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            122 KISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 48.31
Matches 69, Conservative
                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                    US-08-480-604A-28
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STATE: CA
COUNTRY:
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316 LENLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW 974
                                                                                                                                                                                                                                                                      2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                                                                                                   62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANNEYTIIDCIRNNNSGW
                                                                                                                                                                        Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, USHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTIONS: PREVENTION OF C. DIFFICILE DISEASE CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           Indels
                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                          Query Match
49.2%; Score 378.5; DB 1
Best Local Similarity 48.3%; Pred. No. 5.8e-31;
Matches 69; Conservative 31; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN PRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 05-OCT-1994
FILING DATE: 05-DEC-1993
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1989
FILING DATE: 31-OCT-1989
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 KISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            975 KVSLNYGEIIWTLQDTQEIKQRV 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALIFORNIA: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/08915136 Patent No. 6290960 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PARIOR APPLICATION DATA:
PAPPLICATION NUMBER: 08/480,604
FILING DATE:
1296 amino acids
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CARROLL, PETER G.
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US-08-480-604A-23
                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKPIDISGYGSNISINGDVYIYSTNRNQFG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/09084517
; Sequence 28, Application US/09084517
; Patent No. 661329
; GENERAL INFORMATION: VACCINE AND APPLICANT: WILLIAMS, JAMES A.
APPLICANT: WILLIAMS, JAMES A.
ITILE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
STREET: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                   DB 2; Length 1296;
                                                                                                                                                                                                                                                                                                        42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTEY: UNITED STATES OF AMERICA
ZIP: 94104
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                 ch 49.2%; Score 378.5; DB 2
1 Similarity 48.3%; Pred. No. 5.8e-31;
69; Conservative 31; Mismatches 42
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMINICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-838
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-DEC-1993
RICA APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           975 KVSLNYGEIIWTLQDTQEIKQRV 997
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02-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                    / MOLECULE TYPE: protein US-08-915-136-28
                                                                                                                                                                          amino acid
                                                                                                                                                                                              linear
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                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-084-517-28
                                                                                                                                                                                                                                                                       Query Match
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Sequence 219, Application US/10360101

Sequence 219, Application US/10360101

Sequence 219, No. 68612336

GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way FILE REFERENCE: 2103-5673

CURRENT APPLICATION NUMBER: US/10/360,101

CURRENT APPLICATION NUMBER: EP 2007-060.8

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 309

SOFTWARE: Patentin version 3.1

SEQ ID NO 219

LENGTH: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: sequence A-heavy chain of clostridium botulinum toxin type A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGW 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
                                                                                                                                                                                                                                                                                                                                                                     2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG
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                                                                                                                                                                                                                                                                                    Length 1296;
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Best Local Similarity 49.0%; Pred. No. 4.2e-31;
Matches 70; Conservative 29; Mismatches 43;
                                                                                                                                                                                                                                                                                                          .8e-31
                                                                                                                                                                                                                                                                                    49.2%; Score 378.5; 48.3%; Pred. No. 5.8e tive 31; Mismatches
                        OPHD-01610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 KISLNYNKIIWTLODTAGNNOKL 144
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KVSLNYGEIIWTLQDNKQNIQRV 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KISLNYNKIIWTLODTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 975 KVSLNYGEIIWTLQDTQEIKQRV 997
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                       : 1296 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-360-101-219
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23, Application US/08480604A

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NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 438 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94104
                                                                                                                                                          US-08-405-496A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-405-496A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PRCA, JOSEPH N.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STEDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

48.2%; Score 371.5; DB 1; Length 438;
Best Local Similarity 49.6%; Pred. No. 7.6e-31;
Matches 68; Conservative 28; Mismatches 40; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: CALLYCKALA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
ZIP: 94104
ZIP: 94104
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHALIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/422,711
APPLICATION NUMBER: US 08/422,711
APPLICATION NUMBER: US 08/405,496
FILING DATE: 14-APR-1995
RATOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 05-OCT-1994
BADLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 01-OCT-1989
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 01-OCT-1989
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: OPHD-01763
TEREFERENCE/DOCKET NUMBER: OPHD-01763
TERECOMMUNICATION INFORMATION:
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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Sequence 23, Applicati
Patent No. 5736139
GENERAL INFORMATION:
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64 SKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTINNCM-ENNSGWKVSLNY 122
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48.2%; Score 371.5; DB 1; Length 438;
Best Local Similarity 49.6%; Pred. No. 7.6e-31;
Matches 68; Conservative 28; Mismatches 40; Indels 1
Sequence 23, Application US/08405496A
| Sequence 23, Application US/08405496A
| Patent No. 5919665
| GENERAL INFORMATION: WILLIAMS, JAMES A.
| TITLE OF INVENTION: WACCINE FOR CLOSTRIDIUM BOTULINUM
| TITLE OF INVENTION: WEUROTOXIN
| NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: MEDLEN & CARROLL, LLP
| STREET: 220 MONTGOMERY STREET, SUITE 2200
| CITY: SAN FENCISCO
| STATE: CALIFORNIA
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TIVE: FLODRY GIBER
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLEASIFICATION: 424
PRICA APPLICATION DATA:
APPLICATION NUMBER: US/08/329,154
FILING DATE: 25-OCT-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DBC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DBC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTONEY/AGENT INFORMATION:
ANDE: FILING DATE: 31-OCT-1989
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 NKIIWTLODTAGNNOKL 144
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123 GEIIWTLQDTQEIKQRV 139
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                                                                                                                                                                                                                                                                                                         APPLICANT: KINK, JOHN A.
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
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49.6%; Pred. No. 7.6e-31;
trive 28; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 20 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
CITY: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDLUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 25-OCT-1994
APPLICATION DATA: 02-DEC-1993
FILING DATE: 02-DEC-1993
FILING DATE: 02-DEC-1993
APPLICATION DATA: 07/985,321
FILING DATE: 04-DEC-1992
PRICA PAPLICATION DATA: 07/985,321
FILING DATE: 04-DEC-1992
PRICA PAPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 31-OCT-1989
ATTONNEY, AGENT INPORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 09HD-01610
TELECOMMUNICATION: (415) 705-8410
                                                                                                                                                                                                           Sequence 23, Application US/09084517
Patent No. 6613329
GENERAL INFORMATION:
                                                        123 GEIÍWTLÓDTOEIKÓRV 139
128 NKIIWTLQDTAGNNOKL 144
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
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                                                                                                                                                         RESULT 9
US-09-084-517-23
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APPLICANT: FIANLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
TILLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT TITLE OF INVENTION: YERVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 48.2%; Score 371.5; DB 2; Best Local Similarity 49.6%; Pred. No. 7.6e-31; Matches 68; Conservative 28; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PILING DATE:
APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TORNEY/AGENT INFORMATE.
NAME: INGOLIA, DIANTE E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALIFORNIA: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
   US-08-915-136-23
; Sequence 23, Application US/08915136
; Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 705-8410
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94104
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                                                                                    68 SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08405496A
Patent No. 5919665
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURREALING SISIEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 1N-OCT-1989
ATTORING/ADATE: 1N-OCT-1989
ATTORING/ADATE: 40-OCT-1989
ATTORING/ADATION NUMBER: OPHD-01308
TELEPHONE: 41-OCT-1889
ATTORING/ADATION: TELEPHONE: 41-OCT-1889
ATTORING/ADATION: TELEPHONE: 41-OCT-1889
ATTORING/ADATION: TELEPHONE: 41-OCT-1889
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49.6%; Pred. No. 8.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.6%; Prec. ...
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: PATENTIN Release #1
                                                                                                                                                                                                                                              128 NKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338
FORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 amino acids
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Best Local Similarity 49.69
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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INFORMATION F
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                                                                                                                                                                                                             Sequence 26, Application US/08480604A

Patent No. 5736139

GENERAL INPORANTION:
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PARANTE ADDITE, NISHA V.
APPLICANT: STAFFORD, DOUGLAS C.
ITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMENY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%; Score 371.5; DB 1; Length 462; 49.6%; Pred. No. 8.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: PALOABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN PC compatible
COMPUTER: PELOPSY disk
COMPUTER: PELOPSY disk
COMPUTER: PELOPSY disk
COMPUTER: PER PC compatible
COMPUTER: PER PC-DOS/MS-DOS
SOFTWARE: PELOTION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-APR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: APPLICATION NUMBER: US 07/985,321
FILING DATE: APPLICATION NUMBER: US 07/985,321
FILING DATE: APPLICATION NUMBER: US 07/985,321
FILING DATE: APPLICATION NUMBER: US 07/985,321
FILING DATE: APPLICATION NUMBER: US 07/429,791
FILING DATE: APPLICATION NUMBER: US 07/429,791
FILING DATE: APPLICATION NUMBER: US 07/429,791
FILING DATE: APPLICATION NUMBER: US 07/429,791
FILING DATE: APPLICATION NUMBER: US 07/429,791
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FILING DATE: APPLICATION NUMBER: US 07/429,791
FILING DATE: APPLICATION NUMBER: US 07/429,791
FILING DATE: APPLICATION NUMBER: US 07/429,791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REPERBNCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALIFORNIA : UNITED STATES OF AMERICA
                     128 NKIIWTLODTAGNNOKL 144
                                                                           123 GEIÍWŤĽÓDŤQEIKÓRV 139
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 68; Conserva
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STATE: CA
COUNTRY:
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SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127
                8 LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
                                   28 LLSTFTEYIKNIINTSIINLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLES 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IndelB
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49.6%; Pred. No. 8.2e-31;
tive 28; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONIFOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLUASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-WAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION NUMBER: US 08/329,154
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-07-1989
ATTORNEY AGENT INFORMATION:
NAMB: CARROLL, PETER G
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: OPHD-01610
TELEPHONE: (415) 705-9410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
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ZIP.
ZIP.
ZONPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
MCDMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/09084517
Patent No. 6613329
GENERAL INFORMATION:
                                                                                                                                                                                                                                     128 NKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            JS-09-084-517-26
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Gaps
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                                                                                                                                                                                                                                                                                                  APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLEAS C.
APPLICANT: STAFFORD, DOUGLEAS C.
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.2%; Score 371.5; DB 2;
49.6%; Pred. No. 8.2e-31;
iive 28; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,027
REGISTRATION NUMBER: 40,027
REGISTRATION NUMBER: 40,027
REGISTRATION NUMBER: 40,027
REGISTRATION NUMBER: 00PD-01763
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                             Sequence 26, Application US/08915136
Patent No. 6290960
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                   128 NKIIWTLODTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.6
Matches 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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US-08-915-136-26
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62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDÇIRNNN 118
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                                                                                          SEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNY 127
                          28 LLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLES 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
8 LILYFUKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 2-ANG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 2-ANG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 2-DEC-1996
ATTORNEY/AGENT IRFORMATION:
NAME: ESMOND, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
F: 1100 NEW YORK AVENUE, NW, SUITE 600
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CONDESSONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.1%; Score 355; DB 2;
47.3%; Pred. No. 1.5e-28;
tive 33; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09255829 Patent No. 6461617
                                                                                                                                                                                  128 NKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1169 amino acids
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Best Local Similarity
Matches 69; Conservat
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APPLICANT: Mol1, Gert N.
APPLICANT: Mol1, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
RIDEATE APPLICATION NUMBER: BP 02077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SEQ ID NO 220
LENGTH: 1290
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.1%; Score 355; DB 2; Length 12 Best Local Similarity 47.3%; Pred. No. 1.7e-28; Matches 69; Conservative 33; Mismatches 38; Indels
960 SGWKISIRGNRIIWTLIDINGKTKSV 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | | | | : | : | | | | | | | : : | SGWKISIRGNRIIWTLIDINGKTKSV 984
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                                                                                                              Sequence 220, Application US/10360101
Patent No. 6861236
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: March
Job time : 18.7077 secs
                                                                                              US-10-360-101-220
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                                                                                          2, 2006, 01:11:03; Search time 57.2993 Seconds (without alignments) 1050.055 Million cell updates/sec
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                                                                                                                                                                                         1 SYTNDKILILYFNKLYKKIK......LNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA_Main:*
| / cgn2 6/prodata/1/pubbaa/USO7_PUBCOMB.pep:*
2: / cgn2 6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: / cgn2 6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
4: / cgn2 6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
5: / cgn2 6/prodata/1/pubpaa/USIOB_PUBCOMB.pep:*
6: / cgn2 6/prodata/1/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-130-973A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-10-130-973A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-130-973A-14
-10-478-516-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-452-024-152
-10-205-516-12
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-130-973A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10-130-973A-4
                                                                                                                                                                                                                                                                    1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
                                                                                                                                                        US-08-981-087B-2
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1092
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                                                                                              March
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                                                                                                                                                           Title:
Perfect score:
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Maximum DB
                                                                 OM protein
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                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                         Searched:
                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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28 626.5 81.4 1274 4 US-10-729-039-71 Sequence 71, Appl 0626.5 81.4 1274 5 US-10-729-88-71 Sequence 71, Appl 31 626.5 81.4 1274 5 US-10-729-88-71 Sequence 71, Appl 32 626.5 81.4 1274 5 US-10-727-88-71 Sequence 71, Appl 32 626.5 81.4 1274 6 US-11-001-241-71 Sequence 71, Appl 33 625.5 81.2 1280 4 US-10-452-024-162 Sequence 162, Appl 35 593.5 77.1 448 4 US-10-354-774-73 Sequence 73, Appl 36 593.5 77.1 448 4 US-10-21-027-3 Sequence 73, Appl 38 593.5 77.1 448 4 US-10-729-039-73 Sequence 73, Appl 41 593.5 77.1 448 5 US-10-729-039-73 Sequence 73, Appl 42 593.5 77.1 448 5 US-10-729-039-73 Sequence 73, Appl 44 577.1 448 6 US-10-729-66-73 Sequence 73, Appl 44 571.5 74.2 449 5 US-10-728-66-73 Sequence 73, Appl 44 571.5 74.2 449 5 US-10-728-66-73 Sequence 73, Appl 44 571.5 74.2 449 5 US-10-728-68-74 Sequence 73, Appl 44 571.5 74.2 449 5 US-10-234-774-56 Sequence 73, Appl 44 571.5 74.2 449 1 US-10-244-774-56 Sequence 66, Appl 45 571.5 74.2 449 1 US-10-254-774-56 Sequence 56, Appl 45 571.5 74.2 452 4 US-10-254-774-56
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# ALIGNMENTS

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WESULY 1

SEQUENCE 2, Application US/08981087A

SEQUENCE 2, Application US/08981087A

Publication No. US20020091304A1

GENERAL INFORMATION:

APPLICANT: Blucore, Michael J.

APPLICANT: Mauchine, Margaret L.

APPLICANT: Matchink, Vladamir A.

APPLICANT: Titball, Richard W.

APPLICANT: Titball, Richard W.

APPLICANT: Titball, Richard W.

APPLICANT: Titball, Richard W.

APPLICANT: Titball, Richard W.

APPLICANT: Titball, Richard W.

APPLICANT: Titball, Richard W.

APPLICANT: Titball, Richard W.

ADDRESSEE: MIXON & VANDERHYE P.C.

STREET: 1100 No. US20020081304A1th Glebe Rd. 8th floor

CITY: Arlington

STREET: 1100 No. US20020081304A1th Glebe Rd. 8th floor

CITY: Arlington

STREET: 1100 No. US20020081304A1th Glebe Rd. 8th floor

CITY: Arlington

STREET: Arlington

STREET: Arlington

STREET: Arlington

STREET: TANYON WOMBER: US/08/981,087A

FILING DATE: 27-MAY-1998

CURRENT APPLICATION NUMBER: US-00996/01409

FILING DATE: 12-UN-1996

APPLICATION NUMBER: 12-UN-1996

APPLICATION NUMBER: 12-UN-1996

APPLICATION NUMBER: 12-UN-1996

APPLICATION NUMBER: 25,327

REGISTRATION TOWER: 25,327

RESIDENCY: 1100

INFORMATION FOR EGO ID NO: SEGURAL SELECT SELEPAN: 703-816-4100

INFORMATION FOR EGO ID NO: SEGURAL SELEPAN: 703-816-4100

INFORMATION FOR EGO ID NO: SEGURAL SELEPAN: 703-816-4100

INFORMATION FOR EGO ID NO: SEGURAL SELEPAN: TOPOLOGY: Linear

TOPOLOGY: Linear

MODOLOGY: Linear

MODOLOGY: THE PEDEL TOPOLOGY: TINEAR

MODOLOGY: THE PEDEL TOPOLOGY: Linear

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61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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| Sequence 16, Application US/09910186A
| Publication No. US2003009025A1
| GENERAL INFORMATION:
| APPLICANT ORANITON: RECOMBINANT VACCINE AGAINST BOTULINUM
| TITLE OF INVENTION: NEUROTONIN
| TITLE OF INVENTION: NEUROPAIN
| FILE REFERENCE: A33626-A 067252.0107
| CURRENT FILING DATE: 2001-07-20
| PRIOR PELICATION NUMBER: US/09/910,186A
| PRIOR PELICATION NUMBER: 09/611,419
| PRIOR PELICATION NUMBER: 60/133,865
| PRIOR PELING DATE: 1999-05-12
| PRIOR PELING DATE: 1999-05-12
| PRIOR PELING DATE: 1999-05-12
| PRIOR PELING DATE: 1999-05-12
| PRIOR PELING DATE: 1999-05-12
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| PRIOR PELING DATE: 1999-05-12
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                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIFICATION NUMBER: US/08/981,087A
FILING DATE: 12-MN-1998
FILING DATE: 12-JUN-1996
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
FILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CTAMFORM ATTORNEY
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 124-688
TELLEPHONE: 103-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 770; DB 2;
Pred. No. 4.3e-64;
Mismatches 0;
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                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.0%;
Matches 144; Conservative 0
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                                   ZIP: 22201-4741
COMPUTER READABLE FORM:
                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                           MEDIUM TYPE:
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                                                                                                                 COMPUTER:
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APPLICANT: Simpson, Lance
APPLICANT: Park, Jung-Beak
APPLICANT: Park, Jung-Beak
TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-9601
CURRENT APPLICATION NUMBER: US/10/452,024
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: 60/384,949
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin version 3.2
SEQ ID NO 173
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                                                                                                                                                                                                                                                   61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
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        Length 144;
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APPLICANT: Minton, Nigel P.
APPLICANT: Pasechnik, Vladimir A.
APPLICANT: Titball, Richard W.
TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US200200081304Alth Glebe Rd. 8th floor
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     100.0%; Score 770; DB 2;
100.0%; Pred. No. 1.2e-64;
ive 0; Mismatches 0;
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100.0%; Pred. No. 3.5e-64;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Clostridium botulinum
Query Match
Best Local Similarity 100.
Matches 144, Conservative
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Best Local Similarity
Matches 144; Conserva
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US-08-981-087A-1
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100.0%; Score 770; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.3e-64;
Matches 144; Conservative 0; Mismatches 0; Indels (
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TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:

HILE REPERENCE: A33626-A 067252.0107
CURRENT APPLICATION NUMBER: US/09/910,186A
CURRENT PILING DATE: 2001-07-20
PRIOR PAPLICATION NUMBER: PCT/US00/12890
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 60/13,865
PRIOR APPLICATION NUMBER: 60/13,865
PRIOR APPLICATION NUMBER: 60/13,865
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
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PRIOR PILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1993-09-21
NUMBER OF SEQ ID NOS: 34
PRIOR PRESEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 34
PRINGER OF SEQ ID NOS: 34
PRINGER PRESEQ FOR WINGOWS VERSION 4.0
PRIOR APPLICATION NUMBER: 60/133,869
PRIOR FILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/133,873
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1993-09-21
PRIOR FILING DATE: 1993-09-21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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US-09-910-186A-34
                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic Construct
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                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Length 432;

DB 3;

100.0%; Score 770;

Query Match

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APPLICANT: Simpson, Lance
APPLICANT: Bark, Jung-Beak
APPLICANT: Bark, Jung-Beak
APPLICANT: Maksymowych, Andrew
TITLE OF INVEXTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-9611
CURRENT APPLICATION WINBER: US/10/452,024
CURRENT APPLICATION NUMBER: 60/384,949
PRIOR APPLICATION NUMBER: 60/384,949
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin version 3.2
SEQ ID NO 178
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APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT APPLICATION NUMBER: PCT/GB00/04644
PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1990-12-07
PRIOR FILING DATE: 1990-12-07
PRIOR FILING DATE: 1990-12-07
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Pred. No. 4.3e-64;
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Best Local Similarity 100.0%; Pred. No. 4.3e-64;
Matches 144; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 144; Conservative 0
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GENERAL INFORMATION:
APPLICANT: Shone, Clifford
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RESULT 8
US-10-478-516-5
; Sequence 5, Application US/10478516
; Publication No. US2004020889A1
; GENERAL INFORMATION:
; APPLICANT: Suton, John M.
; APPLICANT: Shone, Clifford C.
; TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
; TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
; CURRENT PILLOR DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: PCT/GB02/02384
; PRIOR FILLING DATE: 2002-05-21
; PRIOR FILLING DATE: 2002-05-21
; PRIOR PAPLICATION NUMBER: GB 0112687.9
; RIOR FILLING DATE: 2001-05-24
; SOFTHARE: Patentin Version 3.1
; SEQ ID NOS: 32
; SOFTHARE: Patentin Version 3.1
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100.0%; Score 770; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.9e-64;
Matches 144; Conservative 0; Mismatches 0;
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100.0%; Score 770; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.9e-64;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                             ) OTHER INFORMATION: synthetic construct US-10-130-973A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 WKISLNYNKIIWTLQDTAGNNOKL 144
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial sequence
                                       SEQ ID NO 8
LENGIH: 645
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Sequence 6, Application US/10478516; Publication No. US200402088899A1

US-10-478-516-6

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; OTHER INFORMATION: thrombin linker, diphtheria toxin translocation domain, BoNT/F-HO
US-10-478-516-6
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US-10-478-516-7
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Publication Wo. US2004020889A1
GENERAL INFORMATION;
APPLICANT: Sutcon, John M.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins;
FILE REPRENCE: 1581.1000000
CURRENT FILING DATE: 2003-11-24
FRIOR APPLICATION NUMBER: PGT/GB02/02384
FRIOR APPLICATION NUMBER: PGT/GB02/02384
FRIOR APPLICATION NUMBER: GB 0112687.9
FRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARR: Patentin Version 3.1
SEQ ID NO
                   APPLICANT: Sutton, John M.

APPLICANT: Shore, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REFERENCE: 1581.1000000
CURRENY APPLICATION WHWER: US.10/478,516
CURRENY FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: PCT/GB02/02384
PRIOR APPLICATION NUMBER: GB 0112687.9
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
SOFTWARE: Patentin Version 3.1
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100.0%; Score 770; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 7e-64;
Matches 144; Conservative 0; Mismatches 0; Indels
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Matches 144; Conservative 0
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ORGANISM: Artificial sequence
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             LENGTH: 657
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APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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; Pred. No. 9.7e-64;
0; Mismatches 0;
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100.0%; Score 770; DB 4;
Best Local Similarity 100.0%; Pred. No. 7.4e-64;
Matches 144; Conservative 0; Mismatches 0;
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PRIOR PILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PET/GB00/04644
PRIOR RPILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOUTWARE: Patentin version 3.0
SEQ ID NO 4
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                                                                         FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-130-973A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKISLNYNKIIWTLQDTAGNNOKL 144
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Best Local Similarity 100.0%;
Matches 144; Conservative 0
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                        TYPE: PRT
ORGANISM: Artificial
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US-10-130-973A-4
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APPLICANT: Sutcon, John
APPLICANT: Sutcon, John
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.092000
CURRENT APPLICATION UMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sutton, John
APPLICANT: Sutton, John
APPLICANT: Sliman, Nigel
TITLE SILENDER STATE STATE STATE STATE
TITLE REFERENCE: 1581.092000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR PILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/CBB0/04644
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
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287 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 346
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PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: GB 9228530.6
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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                                                         121 WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                     Sequence 12, Application US/10130973A Publication No. US20030147895A1
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ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
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APPLICANT: Shone, Clifford
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GENERAL INFORMATION:

APPLICANT: Shone, Clifford
APPLICANT: Structon, John
APPLICANT: Structon, John
TITLE OF INVENTION: CONStructs for Delivery of Therapeutic Agents to Neuronal Cells
TITLE OF INVENTION: CONStructs for Delivery of Therapeutic Agents to Neuronal Cells
TITLE OF INVENTION CONSTRUCTS 1881.02920000
CURRENT APPLICATION NUMBER: US/10/130,973A
THIOR APPLICATION NUMBER: PS/000/04644
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
SERVICE OF SEQ ID NOS: 18
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Sequence 26, Application US/10478516

Publication No. US20040208889A1

GENERAL INFORMATION:

APPLICANT: Sutton, John M.

APPLICANT: Shone, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REPERENCE: 1581.1000000

CURRENT APPLICATION NUMBER: US/10/478,516

FRIOR APPLICATION NUMBER: PCT/GB02/02384

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Version 3.1
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100.0%; Score 770; DB 4; Length 887;
Best Local Similarity 100.0%; Pred. No. 1e-63;
Matches 144; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 770; DB 4; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.1e-63;
Matches 144; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial sequence
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Best Local Similarity
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US-10-478-516-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-478-516-26
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LENGTH: 979
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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60

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Db 549 SYTNDKILLIZFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 608

Qy 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANBEYTIIDCIRNNNSG 120

Db 609 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANBEYTIIDCIRNNNSG 668

Qy 121 WKISLNYNKIIWTLQDTAGNNQKL 144

Db 669 WKISLNYNKIIWTLQDTAGNNQKL 692

Search completed: March 2, 2006, 01:17:47

Job time: 57.2993 secs
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2, 2006, 01:12:18; Search time 5.84687 Seconds (without alignments) 491.279 Million cell updates/sec
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770
1 SYTNDKILILYFNKLYKKIK...........LNYNKIIWTLQDTAGNNQKL 144
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USI0_NEW PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USI0_NEW PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USI1_NEW PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                       133702 seqs, 19947517 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		d						
Result No.	Score	Query Match	f Query Match Length	DB	. QI	Description	ផ្ត	
	770	100.0	1059	7	US/11/062	Sequence	5, A	Appl
8	770	100.0	1084	7	US/11/062	Sequence	8,	ppl
	626.5	81.4	838	9	US-10-909-769-28	Sequence	28,	App
4	571.5	74.2	829	9	US-10-909-769-26	Sequence	26,	App
Ŋ	378.5	49.2	849	9	US-10-909-769-18	Sequence	18,	App
9	378.5	49.2	1067	7	US/11/062	Sequence	3, A	[dd
7	378.5	49.2	1092	7	US/11/062	Sequence	6, 4	Appl
8	355	46.1	1070	7	1,	Seguence	4, 4	pp]
6	355	46.1	1095	7	US/11/062	Sequence	٦, ٦	ppJ
10	355	46.1	1169	7	H	Sequence	20,	App
11	348	45.2	900	9	US-10-909-769-20	Sequence	20,	App
12	319	41.4	855	9	US-10-909-769-30	Sequence	30,	App
13	250	32.5	842	9	US-10-909-769-22	Sequence	22,	App
14	249.5		834	9	US-10-909-769-24	Sequence	24,	App
15	206		1315	7	US-11-077-550-141	Sequence	141,	Ap
16	85	11.0	3194	7	=	Sequence	90,	App
17	81	10.5	347	7	Ξ	Sequence	10240	o,
18	77.5	10.1	751	7	US-11-052-554A-109	Sequence	109,	Ą
19	76.5	6.6	443	7	US-11-036-532A-131	Sequence	131,	Ap
20	76.5	6.6	1332	7	US-11-091-643-18	Sequence	18,	App
21	76.5	6.6	1340	7	US-11-070-575-6	Sequence	, ,	\pp]
22	75.5	8.6	357	7	US-11-087-099-3020	Sequence	3020, A	٠,
23	75.5	9.6	923	7	US-11-057-058-66	Sequence	99	App
24	75.5	9.6	1344	7	US-11-091-643-20	Sequence	20,	Apr
25	75	9.7	182	9	US-10-793-626-2414	Sequence	241	٠ `

RESULT 2 US/11/062

# ALIGNMENTS

RESULT 1 US/11/062 ; Sequence 5, Publication GENERAL INF APPLICANT: APPLICANT	SULT 1 /11/062 Sequence 5, Application US/11062471A Sequence 5, Application US/11062471A Sublication No. US20050255033A1 GENERAL INFORMATION: APPLICANT: SULTON, John Mark APPLICANT: SULTON, John Mark APPLICANT: SULTON, Nigel TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells FILE REFERENCE: 1581.080001 CURRENT APPLICATION NUMBER: US/11/062,471A CURRENT FILING DATE: 1299-11-05 PRIOR FILING DATE: 1299-11-05 PRIOR FILING DATE: 1999-11-05 PRIOR FILING DATE: 1999-11-05 RRIOR APPLICATION NUMBER: GB 9824282.9 PRIOR FILING DATE: 1998-11-05 NUMBER OF SEQ ID NOS: 11 SECONTANDER: PARCHERICATION NUMBER: GB 9824282.9 NUMBER OF SEQ ID NOS: 11
; LENGTH: 1059; TYPE: PRT ; CRGANISM: Ar ; FEATURE: ; CTHER INFORM	LENGTH: 1059 TYPE: RT PORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker, 17,062, 471a-5
Query Match Best Local Matches 14	Query Match 100.0%; Score 770; DB 7; Length 1059; Best Local Similarity 100.0%; Pred. No. 3.1e-63; Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
6 5 6	1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60 
è 4	61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLANEYTIIDCIRNNNSG 120 
Oy 10	121 WKISLNYNKIWTLODTAGNNOKL 144                        749 WKISLNYNKIIWTLODTAGNNOKL 772

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Sequence 26, Application US/10909769
; Sequence 26, Application US/10909769
; Publication No. US20060024331A1
; GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Lin, Wei-Jen
APPLICANT: Sachs, George
APPLICANT: Sachs, George
TITLE OF INVENTION: TOXIN Compounds with Enhanced Membrane Translocation Characterist
FILE REPERENCE: ALLEO10-100 (RO12003-146)
CURRENT FLING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 26
LENGTH: 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stewands-Salas, Ester
APPLICANT: Stewands, Lance E.
APPLICANT: Stewand, Lance E.
APPLICANT: Stewand, Lance E.
APPLICANT: Stewand, Lance E.
APPLICANT: APPLICANT: APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteris
FILE REFERENCE: ALLEGO10-100 (ROI2003-146)
CURRENT PEPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 18
LENGTH: 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GIYSSKRSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNK-VNLANNEYTIIDCIRNNNS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 SYTDDKILISYFNKFFKRIKSSSVLAMRYKANDKYVDTSGYDSNININGDVYKYPTNKNQF
                                                                                 61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.2%; Score 571.5; DB 6; 71.7%; Pred. No. 4.2e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Amino acid sequence of HC
                                                                                                                                                                                   121 WKISLNYNK---IIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                  531 WKISLRTVRDCEIIWTLQDTSGNKENL 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GWKISLNYNKIIWTLQDTAGNNQKL 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SUTTON, JOHN MARK
APPLICANT: SUTTON, JOHN MARK
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
TILLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 2005-02-22
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
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SPRIOR PLILING DATE: 1998-11-05
SPRIOR PLILING DATE: 1998-11-05
SPRIOR PLILING DATE: 1998-11-05
SUTURARE: PATENTIN NUMBER: CENTRAL SUPERIOR DELIVERY OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 770; DB 7; Length 1084; 100.0%; Pred. No. 3.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
81.4%; Score 626.5; DB 6; Length 9
Best Local Similarity 80.3%; Pred. No. 3.8e-50;
Matches 118; Conservative 14; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 WKISLNYNKIIWTLQDTAGNNOKL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 28, Application US/10909769; Publication No. US20060024331A1; GENERAL INFORMATION: APPLICANT: Pernandez-Salas, Ester
Sequence 8, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
                                                                                 APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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1 SYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQF 60

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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M
US/11/062,471A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, John Mark
APPLICANT: SHONE, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT PILING DATE: 2005-02-22
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: O9/831,050
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENT ON SEC ID NOS: 11
SOFTWARE: PATENT OF SEQ ID NOS: 11
SOFTWARE: PATENT OF SEQ ID NOS: 11
SEQ ID NO 4
SEQ ID NOS: 12
                                       APPLICANT: SILLAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT APPLICATION NUMBER: US/831,050
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR FILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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46.1%; Score 355; DB 7; Length 1070;
Best Local Similarity 47.3%; Pred. No. 4.6e-25;
Matches 69; Conservative 33; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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ORGANISM: Artificial Sequence
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SUTTON, John Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687 LPNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGW 745
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                                                                                                                                                                                                                                                         APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT APPLICATION NUMBER: PCT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR PLING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SOPTWARE: PATENTIN VET. 2.1
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                                                                                                             Query Match

49.2%; Score 378.5; DB 6; Length
Best Local Similarity 48.3%; Pred. No. 2.4e-27;
Matches 69; Conservative 31; Mismatches 42; Indels
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             ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 KISLNYNKIIWTLODTAGNNOKL 144
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KVSLNYGEIIWTLQDTQEIKQRV 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/11062471A Publication No. US20050255093A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHONE, Clifford Charles
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1067
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Sequence 20, Application US/10909769;
Factoria 20, Application US/10909769;
Publication No. US20060024331A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Acki, Kei Roger
APPLICANT: Acki, Kei Roger
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: 10xin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: 2010-100 (ROIZ2003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20
LENGTH: 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 46.1%; Score 355; DB 7;
1 Similarity 47.3%; Pred. No. 5.1e-25;
69; Conservative 33; Mismatches 38
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45.2%; Score 348; DB 6;
Best Local Similarity 45.6%; Pred. No. 1.7e-24;
Matches 67; Conservative 35; Mismatches 39.
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                                                                    CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION WUMBER: 10/241,596
PRIOR FILING DATE: 2002-09-12
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1996-12-27
PRIOR PILING DATE: 1996-12-27
PRIOR FILING DATE: 1996-12-33
PRIOR FILING DATE: 1996-08-23
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 179
SEQ ID NO 20
                                                 US/11/077,550
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; ORGANISM: Clostridium botulinum
US-11-077-550-20
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 69; Conserv
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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human
US/11/062,471A-7
                                        62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/11062471A
Publication No. US20050255093A1
GENERAL INFORMATION:
APPLICANT: SUTTON, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPRENCE: 1281.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
FILE OF INVENT APPLICATION NUMBER: US/11/062,471A
FRIOR APPLICATION NUMBER: US/11/05
FRIOR PILING DATE: 1999-11-05
FRIOR PILING DATE: 1999-11-05
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APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Poster, Keith Alan
APPLICANT: Chaddock, John
APPLICANT: Marks, Philip
APPLICANT: Sutcom, J. Mark
APPLICANT: Stancombe, Patrick
APPLICANT: Stancombe, Patrick
APPLICANT: Rayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
                                                                                                                                                                                                                                                                            739 SGWKISIRGNRIIWTLIDINGKTKSV 764
                                                                                                                                                                                                                                      119 SGWKISLNYNKIIWTLQDTAGNNOKL 144
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Publication No. US20050244435A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 69; Conservat
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US-11-077-550-20
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APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Lin, Wei-Jen APPLICANT: Lin, Wei-Jen APPLICANT: Lin, Wei-Jen APPLICANT: Aoki, Kei Roger APPLICANT: Aoki, Kei Roger APPLICANT: Sachs, George TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist FILE OF PREFERENCE: ALLEGOID-100 (ROIZ003-146) CURRENT APPLICATION NUMBER: US/10/909,769 CURRENT PILING DATE: 2004-08-02 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin version 3.3 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463
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  Length 842;
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32.5%; Score 250; DB 6; 37.7%; Pred. No. 1.6e-15; iive 30; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Amino acid segence of HC US-10-909-769-24
                                                                                                                                                                                                                                                                       119 SGWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                                                                                                                                                                                                              517 SGWSIGIISNFLVFTLKQNEDSEQSI 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 WKISLNYNKIIWTLQDTAGNNOK 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 141, Application US/11077550
Publication No. US20050244435A1
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fernandez-Salas, Ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                55; Conservative
                       Best Local Similarity
Matches 55; Conserv
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    Query Match
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: ALKSOK, Kei Roger
APPLICANT: ACROSTOR Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
TITLE OF INVENTION: 10x10 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT PILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 842
                                                                                                                                                                                                                                                                                                                APPLICANT: Steward, Lance E. APPLICANT: Steward, Lance E. APPLICANT: Lin, Wei-Jen APPLICANT: Aoki, Kei Roger APPLICANT: Aoki, Kei Roger APPLICANT: Sachs, George TTTLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist FILE REFERENCE: ALLEGOIO-100 (ROIZ003-146) CURRENT APPLICATION NUMBER: US/10/909,769 CURRENT FILING DATE: 2004-08-02 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 IYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFN---KVNLNNEYTIIDCIRNNN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 LANSENSNITAHQSKFVVYDSMFDNFSINFWVRTPKYNNNDIQTYLQNEYTIISCIK-ND 524
    509 KLTSSADSKIRVTQNQNIIFNSMFLDFSVSFWIRIPKYRNDDIQNYIHNEYTIINCMK-N 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 YTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFG 61
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41.8%; Pred. No. 7.3e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Amino acid sequence of HC US-10-909-769-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Mismatches
                                                                            NSGWKISLNYNKIIWTLQDTAGNNQKL 144
                                                                                                   568 NSGWKISIRGNRIIWTLIDINGKTKSV 594
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                                                                                                                                                                                                                             Sequence 30, Application US/10909769 Publication No. US20060024331A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT: Fernandez-Salas, Ester
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LENGTH: 855
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Best Local S
Matches 61
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| CURRENT APPLICATION NUMBER: US/11/077.550
| CURRENT FILING DATE: 2005-03-13
| PRIOR PILING DATE: 2005-03-13
| PRIOR PILING DATE: 2005-09-12
| PRIOR PILING DATE: 1099-0-20-13
| PRIOR PILING DATE: 1999-0-20-13
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Search completed: March 2, 2006, 01:18:29 Job time : 6:84687 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein March 2, 2006, 00:31:42; Search time 68.993 Seconds (without alignments) 917.057 Million cell updates/sec Run on:

US-08-981-087B-3 761 1 VFNYTQMISISDYINKWIFV......ITQNSNFLNINQQRGVYQKP 144

Title: Perfect score: Sequence:

Scoring table:

2443163 seqs, 439378781 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s: geneseqp2005s: geneseqp2004s: geneseqp2001s A\_Geneseq\_21:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Aaw09016 Immunogen	Aaw09014 Immunogen				-		Aae35693 BoNT/F-Hc	_	Aae07893 Modified	Aae07890 Modified	_	_	Aae07901 C. botuli	Aay93309 A mangane	Aay93312 A mangane	Aae07900 C. botuli	Aae35711 BONT/F-Hc	_	Aaw68399 Clostridi				Aaw68396 Clostridi
COLUMNICO	ΩI	AAW09016	AAW09014	AAY77138	AAB04103	AAB04096	AAE07894	AAE35692	AAE35693	AAE35694	AAE07893	AAE07890	AAE07892	AAE35713	AAE07901	AAY93309	AAY93312	AAE07900	AAE35711	AAE35710	AAW68399	AAB04095	AAY77137	AAB04094	AAW68396
	DB	7	7	٣	4	4	4	9	9	9	4	4	4	9	4	٣	e	4	9	9	~	4	٣	4	7
	Length	144	431	432	432	432	645	645	657	657	685	862	887	979	1032	1059	1084	1092	1192	1192	448	419	449	449	452
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	80.4	65.4	65.4	65.4	65.4
	Score	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	761	612	497.5	497.5	497.5	497.5
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Aaw68395 Clostridi Aae07898 Modified			Aay77142 Native bo		Aab04088 Botulism	Aar95008 Type A ne		٠,		Aar95009 Type A ne		_			-	Aau99339 Clostridi
AAK68395 AAE07898	AAB35303 ADW24418	ADZ60271 ADZ60276	AAY77142	AAB04089 AAB04090	AAB04088	AAR95008	AAW68389	AAY77134	AAW68391	AAR95009	AAW68390	AAY77140	ADZ69764	AAY93307	AAY93310	AAU99339
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451	382	382 425	432	434 435	437	438	438	438	445	462	462	837	859	1067	1092	1295
65.1	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	,57.9	57.9	57.9	57.9	57.9	57.9
495.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5
25	27 28	30 30	31	32	3.4	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism. Immunogenic type F botulinum toxin polypeptide (aa992-1135). Clostridium botulinum; type F strain Langeland AAW09016 standard; protein; 144 AA (first entry) (revised) 17-OCT-2003 31-MAR-1997 AAW09016; AAW09016

96WO-GB001409. WO9641881-A1 12-JUN-1996; 27-DEC-1996.

Elmore MJ, Mauchline ML, Minton NP, Pasechnik VA; (MICR-) MICROBIOLOGICAL RES AUTHORITY 

95GB-00011909.

12-JUN-1995;

Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn. WPI; 1997-065467/06.

Claim 5; Page 18-19; 37pp; English.

Novel polypeptides (AAM09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BONT/F). They lack the L chain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine product Recombinant polypeptides can be produced in transformed host cells, as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 144 AA;

Query Match

100.0%; Score 761; DB 2; Length 144;

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                                                                                                                                                                                                                                                                                        61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                         61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a type F botulinum neurotoxin (BONT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAM09015-17) lack the light chain and HN epitopes necessary for metalloprotesse activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine prodn. Recombinant polypeptides can be produced in transformed host cells, esp. as fusion proteins, e.g. with malcose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                                                                                                                       VENYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                 1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sotulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic type F botulinum toxin heavy chain (aa848-1278).
                                   0; Indels
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       Pred. No. 6.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium botulinum; type F strain Langeland
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minton NP,
                                                                                                                                                                                                                                                                                                                                                                                  TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TDKSITQNSNFLNINQQRGVYQKP 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW09014 standard; protein; 431 AA
100.0%;
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(first entry)
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                                   Matches 144; Conservative
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   Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9641881-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1996;
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31-MAR-1997
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The invention relates to nover vaccines that induce a protective immune response against botulinum neurotosin (BoNT) serotypes A, B, C, D, E, and G (BoNTA-BoNTG). The vaccine of the invention is novel recombinant comprising a vector, and at least one nucleic acid fragment comprising a C-terminal heavy chain fragment (HC) from BoNT serotypes A-G. In preferred embodiments of the invention, the vector is a Venezuelan equine encephalitis vira (VEE) replicon vector. Use of this vector results in the production of large amounts of a protein encoded by a sequence cloned into the replicon. The constructs are used to produce vaccines against botulism. The proteins can also be used as diagnostic tools for the diagnosis of botulism. The transformed host cells can be used to analyse the effectiveness of drugs and agents which inhibit toxin effects. The vaccine currently used against botulism is dangerous and effects. The vaccine is incomplete, in that only 5 of the 7 serotypes are represented in the formulation. The novel vaccine of serotypes are represented in the formulation. The novel vaccine of serotypes are represented in the formulation. The novel vaccine of immune response. Sequences AAY77134-Y77139 represent synthetic BoNT HC fragments used in the present invention. The DNA encoding these sequences had been optimised for codon usage for expression in yeast. Note: This sequence is not given on pages 45-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botulinum neurotoxin; heavy chain; BoNT; serotype F; C-terminal fragment; Venezuelan equine encephalitis virus replicon; VBE; botulism; vaccine; diagnosis; drug screening.
                                            205 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLR 264
VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Botulinum neurotoxin vaccine comprising a fragment from botulinum toxin serotypes A \cdot G_{\nu} is used for inducing an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to novel vaccines that induce a protective immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic botulinum neurotoxin serotype F (BoNTF) C-terminal fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith JF, Parker M, Dertzbaugh MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
                                                                                                                                      TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                     AAY77138 standard; protein; 432 AA.
                                                                                                                                                                                              TDKSITQNSNFLNINQQRGVYQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Page; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US015570
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99US-0133870P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum
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N-PSDB; AAZ87216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-1999;
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145 VENYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI

1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI

Matches 144, Conservative

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Gaps

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Query Match Best Local (

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Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a dichain and as 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encocing the carboxy-terminal (HC) or amino terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT)
to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G
                                                                                                                                                                                                                                                                                                          206 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDFSILKDFWGNYLLYNKRYYLLNLLR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding the carboxy- or amino-terminal portions of theavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                                                                                                                                                                                                   61 VGCNDTRYVGIRYFKVFDTBLGKTBIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                                                                                                                                                           1 VENYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                  Length 432;
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lapenotiere H;
                                                                                                                              / Match 100.0%; Score 761; DB 4; Local Similarity 100.0%; Pred. No. 2.6e-73; nes 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND
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                                                                                                                                                                                                                                                                                                                                                                                             TDKSITONSNFLNINOORGVYOKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB04096 standard; protein; 432 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0133865P.
99US-0133866P.
99US-0133867P.
99US-0133868P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith LA, Byrne MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-016048/02.
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                                                                                                  Sequence 432 AA;
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12-MAY-1999;
29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                           266
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                                                                                                                                        Query Match
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Matches
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                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                                                                                                        205
                                                                                                                                                                                                     61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                          VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                   ö
                               Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botulism toxin heavy chain C-terminal sequence (serotype F)
                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith LA, Byrne MP, Middlebrook JL, Lapenotiere
                             Score 761; DB 3;
Pred. No. 2.6e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 AAB04103 standard; protein; 432 AA
                               100.0%;
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99US-0133866P.
99US-0133867P.
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99US-0146192P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                     Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium botulinum.
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                                                   Similarity
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29-JUL-1999;
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12-MAY-1999; 12-MAY-1999; 12-MAY-1999;

12-MAY-1999

16-NOV-2000

Synthetic

infection

AAB04103;

AAB04103 ID AABC

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transformed cells to produce peptide antigens useful for eliciting an timmune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                   New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as
                                                                                                                                                                                                                                                                                                                    146 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                     1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                    Length 432;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                    ; Score 761; DB 4;
; Pred. No. 2.6e-73;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified clostridial heavy chain fragment #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                   121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE07894 standard; protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 44; 50pp; English.
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07-APR-2000; 2000GB-00008658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 144; Conservative
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                                                                                                                                                                                        Sequence 432 AA;
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01-NOV-2001
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ID AAE
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Hc) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fushing the binding domain of boculinum neurotoxin type F (BONT)F) with translocation domain of diphtheria neurotoxin. (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGCNDTRYVGIRYFKVFDTELGKTBIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 VENYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 761; DB 4;
100.0%; Pred. No. 4.3e-73;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DipT HN domain-BoNT/F-Hc fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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Clostridium botulinum.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 645 AA;
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17-JUN-2003
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               888888888888888888888888888888888
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a carrier that targets the effector protein to a carrier that targets the effector protein to a carrier that targets the invention is useful for a treatment selected from promoting or inhibiting survival of cells; promoting or inhibiting and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for capting tron disease, Alzheimer' disease and wide range of disorders including muscle spasms such as chronic obstructive pulmonary disease (POPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (Dip HN domain) and botulinum type F neurotoxin from Clostridium function and an expression of field in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 23-OCT-2003 to standardise OS field)
                          Example 12; Page 57-60; 130pp; English.
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Sequence 645 AA;

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                                                                1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                                                                       359 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                    VGCNDTRYVGIRYFKVPDTELGKTELETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                  Gaps
                                  .;
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100.0%; Score 761; DB 6; Length 645; 100.0%; Pred. No. 4.3e-73; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                       121 TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                              Matches 144; Conservative
   Query Match
Best Local Similarity
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AAE35693 standard; protein; 657 AA (first entry) 17-JUN-2003 AAE35693; AAE35693 

BoNT/F-Hc-DipT HN domain-thrombin linker fusion construct.

infection; prion disease, Alzheimer' disease; hypersecretion disorder; muscle spaem; COPP; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain; Apoptosis; therapy; inflammatory mediator; intracellular trafficking; botulinum type F neurotoxin

Corynebacterium diphtheriae. Clostridium botulinum. Unidentified.

WO200296467-A2. Chimeric

05-DEC-2002

21-MAY-2002; 2002WO-GB002384

24-MAY-2001; 2001GB-00012687

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trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as Dephorospasm, torticolis and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corymbacertium diphtheriae toxin translocation domain (Dipt-HN domain), botulinum type F neurotoxin binding domain (BONT/F-HC) from Clostridium botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                             Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                          The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells, killing cells, promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric of a medicament for treating a neuronal is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular
                                                                                                                                                                                                                                                                               Example 12; Page 60-63; 130pp; English.
(MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                          Shone CC;
                                                                                                              WPI; 2003-167247/16.
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430 120 490 9 61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 1 VENYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI Gaps ö 100.0%; Score 761; DB 6; Length 657; 100.0%; Pred. No. 4.4e-73; ive 0; Mismatches 0; Indels C Matches 144; Conservative Query Match Best Local Similarity

TDKSITONSNFLNINQORGVYOKP 144 491 TDKSITQNSNFLNINQQRGVVQKP 514

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AAE35694 standard; protein; 657 AA 17-JUN-2003 (first entry) AAE35694; RESULT 9 AAE35694

BoNT/F-Hc-DipT HN domain-factor Xa linker fusion construct.

Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spaem, CODP, Eronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; funion protein; diphtheria toxin; BONI/F; translocation domain; HN domain; DipT; Hc; binding domain; botulinum type F neurotoxin.

Corynebacterium diphtheriae. Clostridium botulinum. Unidentified. 

Chimeric

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superoxide dismutase; SOD; botulinum neurotoxin type F; BoNT/F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 43; 50pp; English.
                                     Geobacillus stearothermophilus
                                                                                                                                                                                                                                               04-DEC-2000; 2000WO-GB004644.
                                                                                                                                                                                                                                                                                         02-DEC-1999; 99GB-00028530
07-APR-2000; 2000GB-00008658
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Matches 144; Conservative
                                                                               Clostridium botulinum
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                                                             Influenza virus
                                                                                                                                                                  WO200158936-A2.
                                                                                                                                                                                                          16-AUG-2001
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                                                                                                                           Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting substitution and reversing damage to cells; killing cells; promoting or inhibiting and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for thibiting secretion from cells. The invention is also useful for including muscle spasms such as blephorospasm, torticolis and construct comprising Corynabacterium diphtheriae diphtheria toxin translocation domain (DipT-HN domain), botulinum type F neurotoxin binding domain (BoNT/P-HC) from Clostridium botulinum and factor Xa linker peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                        Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 VFNYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 761; DB 6; Length 657; 100.0%; Pred. No. 4.4e-73; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                              Example 12; Page 63-65; 130pp; English.
                                                                                                                                                                                 (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDKSITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 TDKSITQNSNFLNINQQRGVYQKP 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE07893 standard; protein; 685 AA
                                                                                                                                          24-MAY-2001; 2001GB-00012687.
                                                                                              21-MAY-2002; 2002WO-GB002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                           Shone CC;
                                                                                                                                                                                                                                                                   WPI; 2003-167247/16.
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Matches 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 657 AA;
               WO200296467-A2
                                                         05-DEC-2002
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain (amino constructs) and is not a fragment or derivative of domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are collise. The polypeptide constructs are useful for delivering therapeutic calls. The polypeptide constructs are useful to treat disorders of the CC substances to neuronal cells. They are useful to treat disorders of the CC substances to neuronal cells. They are useful to treat disorders of the CC is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase conjugate. This conjugate comprises bacterial Mn-superoxide dismutase (MSOD), from CC translocation peptide from influenza virus and a neuronal cell-specific thinding a neuroperoxine that can be cleaved by factor Xa, thinding a virus and a neuronal cell-specific
                                                                                                                                                                                                                                                                                                                               New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDFSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding domain from botulinum neurotoxin type F (BoNT/F)
(MICR-) MICROBIOLOGICAL RES AUTHORITY.
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AAE07892 standard; protein; 887 AA.

RESULT 12

AAE07892;

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as terminal half of HC, designated as HN), that translocation domain (amino cagent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are a seaful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises bacterial hm.superoxide dismutase (MnSOD), from Bacillus stearothermophilus, linker that can be cleaved by factor Xa, translocation domain from diphtherial neurotoxin and a neuronal cell-cape present sequence capecific binding domain from botulinum neurotoxin type F (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 635
                                                                       Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
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                                    Modified clostridial heavy chain-superoxide dismutase conjugate #2.
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100.0%; Score 761; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.2e-73;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Page 40; 50pp; English.
                                                                                                                                                                      Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2000; 2000WO-GB004644
  (first entry)
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                                                                                                                                                                                                                                                                                            WO200158936-A2.
  01-NOV-2001
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                                                                                                                                                                                                                                                          Chimeric.
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as (carboxy terminal half of heavy chain (HC) of a neurotoxin damino cell, that binds to the neuronal cell and a translocation domain (amino cerminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. They are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are useful to treat disorders of the constructs are also useful lasent therapy. The present sequence of is modified clostridial heavy chain-superoxide dismutase (MNSOD), MNSOD from Bacillus steacothermophilus, clinker that can be cleaved by thrombin, translocation domain from diphtherial neurotoxin and a neuronal cell-specific binding domain from constructs are sequenced betulinum neurotoxin type F (BONT/F)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                   Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VENYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                                                                              Modified clostridial heavy chain-superoxide dismutase conjugate #4.
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Best Local Similarity 100.0%; Pred. No. 6.4e-73;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silman N;
                                                                                                                                                                                                                                                                  Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
Clostridium botulinum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999; 99GB-00028530
07-APR-2000; 2000GB-00008658
                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514643/56.
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                                                           01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                      Synthetic
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, relasse of an inflammatory mediator from cells, division of cells and treating intracellular comparation of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating an neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and chipment observed to observe translocation domain Gorynebacters such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebactersium diphtheriae diphtheriae toxin translocation domain (DipT-HM domain), botulinum type F neurotoxin binding domain (Bory-FHC) from Clostridum botulinum and factor Xa linker peptide and Yersinia pestis targetted effector protien YopT. This sequence is used in
                                                           VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BONT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis; therapy, inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm. COPD, bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; Dipf; HC; binding domain; botulinum type F neurotoxin; targetted effector protien; Yopf.
VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 12; Page 110-114; 130pp; English.
                                                                                                                                                                                                                                                         TDKSITQNSNFLNINQQRGVYQKP 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE35713 standard; protein; 979 AA
                                                                                                                                                                                        121 TDKSITQNSNFLNINQQRGVYQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2001; 2001GB-00012687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sutton JM, Shone CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-167247/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200296467-A2
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                                                                                              661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE35713;
    19
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial coxin. Polypeptides of the invention are caseful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic cells. The polypeptide constructs are useful for delivering therapeutic cells. The polypeptide constructs are useful for terat disorders of the CS ubstances to neuronal cells. They are useful for the invention therapeutic cells they are also useful in gene therapy. The present sequence and infection. They are also useful in gene therapy. The present sequence is C. botulinum c2 entrotoxin translocation domain with botulinum neurodesponents.
                                                                                                           ö
                                                                                                                                                                                                                                                     812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                               752
                                                                                                                                                                                                                 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BONT/F.
                                                                                                                                                                                                                                            753 VGCNDTRYVGIRYFKVFDTBLGKTBIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                                                                                                          1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                                                693 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. botulinum C2 translocation domain with BoNT/F-binding domain #2.
                                                                                                           .
0
                                                                       Length 979;
                                                                                                        Indels
                                                                  100.0%; Score 761; DB 6;
100.0%; Pred. No. 7.3e-73;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                       TDKSITONSNFLNINQORGVYOKP 144
                                                                                                                                                                                                                                                                                                                          836
the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                 AAE07901 standard; protein; 1032 AA
                                                                                                                                                                                                                                                                                                                        TDKSITQNSNFLNINQORGVYOKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 48; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2000; 2000WO-GB004644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-2000; 2000GB-0008658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-514643/56.
                                                                                     Similarity
                                Sequence 979 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200158936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1999;
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                                                                                                    144;
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Best Local
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                                                                                                                                                          VGCNDTRYVGIRYPKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
                                                                                                                                                                                                                                806 VGCNDTRYVGIRYFKVPDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYXLLNLIR 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
                                                                                                                                     9
                                                                                                                                     1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                    ô
                                                               Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell;
                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, Huntington's disease and motor neurone diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A manganese superoxide dismutase (Mn-SOD) construct
                                                         100.0%; Score 761; DB 4;
illarity 100.0%; Pred. No. 7.8e-73;
Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 48-51; 65pp; English
                                                                                                                                                                                                                                                                                                         866 TDKSITQNSNFLNINQQRGVYQKP 889
                                                                                                                                                                                                                                                                                    TDKSITONSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                             AAY93309 standard; protein; 1059 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geobacillus stearothermophilus.
Clostridium botulinum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-376553/32.
                                                                  Query Match
Best Local Similarity
Matches 144; Conserv
                                   Sequence 1032 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200028041-A1
the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000
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1 VENYTOMISISDYINKWIEVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                                 61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR
                                                         0; Gaps
                                Length 1059;
                                                         Indels
                              Query Match
Best Local Similarity 100.0%; Pred. No. 8.1e-73;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                     TDKSITONSNFLNINOORGVYOKP 144
                                                                                                                                                                                                           TDKSITONSNPLNINQORGVYOKP 916
           Sequence 1059 AA;
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2, 2006, 00:38:56 completed: March Search cor Job time

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

- protein search, using sw model OM protein

March 2, 2006, 00:39:17; Search time 12.0278 Seconds (without alignments) 1151.928 Million cell updates/sec Run on:

US-08-981-087B-3 761 1 VFNYTQMISISDYINKWIFV.....ITQNSNFLNINQQRGVYQKP 144 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	DOCULLIUM HEULOCOA	neurotoxin type F	botulinum neurotox	botulinum neurotox	bontoxilysin (EC 3	botulinum neurotox	neurotoxin - Clost	ü	bontoxilysin (EC 3	botulinum neurotox	tentoxilysin (EC 3	botulinum neurotox	botulinum neurotox	botulinum neurotox	progenitor toxin n	botulinum toxin no	nontoxic-nonhemagg	botulinúm neurotox	toxin, nontoxic co	botulinum neurotox	botulinum neurotox	flagellar motor sw	ORF MSV140 hypothe	endo-1,4-beta-gluc	tic	ı	toxin B - Clostrid	cytotoxin L - Clos	probable esterase
			TT	813	S21178	JH0256	BTCLAB	I40645	791	631	A48940	455	BICLIN	777	846431	S70582	A47708	I40817	JC4901	868218	JQ1467	S46430	I40644	H84938	T28301	I40799	AG2560	S10317	870172	40884	97148
	ID		2334TT	I40813	S21	OH5	BIC	140	839791	140631	A48	S11455	BIC	A49777	S46	S70	A47	I40	JC4	868	J01	S46	140	H84	T28	I40	AG2	810	S70	140	B97
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de	Query Match	; ,	81.	80.4	65.4	65.1	57.9	55.7	39.0	38.9	37.4	32.3	31.6	31.4	31.4	29.6	16.7	15.8	15.4	15.2	15.0	15.0	13.8	12.2	12.1	11.8	11.8	11.7	11.7	11.3	11.2
	Score		779	612	497.5	495.5	440.5	423.5	296.5	296	284.5	245.5	240.5	239	239	225	127	120	117	116	114	114	105	92.5	92	•	89.5	89	89	86	82
	Result No.		-	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	DNA-directed RNA p	hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	regulatory protein	protein g377 - mal	hypothetical prote	carbamoy1-phosphat	endo-beta-1,4-gluc	hypothetical prote	26S proteasome reg	multiple banded an	hypothetical prote	rep protein - slim
G71643	RNZQBF	E64240	B71612	T46018	C71610	A33827	T18414	H70103	G84946	JC1299	B84617	G90110	G82923	T19051	A35679
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11.2	11:11	11.0	11.0	11.0	11.0	10.9	10.9	10.8	10.7	10.7	10.6	10.5	10.5	10.5	10.5
ď	84.5	84	84	83.5	83.5	83	83	82.5	81.5	81.5	81	80	80	80	80
90	31	32	33	34	35	36	37	38	39	40	41	42	. 43	44	45

### ALIGNMENTS

RESULT 1

NEOUTL 1
S33411
botulinum neurotoxin type F - Clostridium barati
C,Species: Clostridium barati
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Ju1-2004
C;Accession: S33411; S31860
R; Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.
FEMS Microbiol. Lett. 108, 175-182, 1993
A, Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin
A; Reference number: S33411; MUID: 93252228; PMID: 8486245
A; Accession: S33411
A;Status: preliminary
A; Molecule type: DNA
A;Residues: 1-1268 <tho></tho>
A,Cross-references: UNIPROT:Q45851; UNIPARC:UP100000BAF8C; EMBL:X68262; NID:g49138; PIDN
C;Superfamily: tetanus toxin
C; Keywords: neurotoxin

Gaps . 0 Length 1268; 14; Indels Query Match
Best Local Similarity 79.0%; Pred. No. 3.3e-48;
Matches 113; Conservative 16; Mismatches 14

ö 61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120 09 1 VENYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 셤 ò ò

121 TDKSITQNSNFLNINQQRGVYQK 143 셤 Š 셤

RiBast, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.F. FEMS Microbiol. Lett. 96, 225-230, 1992. A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum. A;Reference number: I40644 neurotoxin type F - Clostridium botulinum C;Species: Clostridium botulinum C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004 C;Accession: I40813; S48108

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1274 <RRS.
A;Croser-references: UNIPROT: P30996; UNIPARC: UPI0000126B8A; GB:M92906; NID:g144866; PIDN
B;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993

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A; Accession: S16145
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Ayesidude
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific id A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48108
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 634-1002 <CAM>
                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP1000016EA7B; EMBL:X70816; NID:g407788; PIDN:CAA50147.1; PI
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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botulinum neurotoxin type E precursor - Clostridium botulinum
C;Species Clostridium botulinum botulinum botulinum
C;Species Clostridium botulinum revision 30-Sep-1993 #text change 31-Dec-2004
C;Accession: S21178; S48107; ŪH0257; B35294; A60027; S18111
C;Accession: S21178; S48107; ŪH0257; B35294; A60027; S18111
Bur. J. Biochem. 204, 657-667, 1992
A;Title: The complete amino acid sequence of the Clostridium botulinum type-E:
A;Reference number: S21178; MUID:92174922; PMID:1541280
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                                                                                                                                                                                                                                                                                                                                                                      ; Score 612; DB 2;
; Pred. No. 2.6e-47;
10; Mismatches 14;
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A;Rcss-references: UNIPARC:UP1000017670F
A;Experimental source: strain Beluga
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                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 82.99
Matches 116, Conservative
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A; Molecule type: protein
A; Residues: 420-427 cdlm
A; Residues: 420-427 cdlm
A; Cross-references: UNIPARC: UPI0000176710
A; Experimental source: strain Beluga
A; Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin
C; Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neu
C; Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig
C; Keywords: neurotoxin
F; H-422, Product: botulinum neurotoxin type E light chain #status predicted <LCH>
F; 412-426/Disulfide bonds: #status predicted
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A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT: P30995; UNIPARC: UPI000017670D; EMBL: X62088; NID: 940379
A; Experimental source: strains ATCC 43181 and ATCC 44755
A; Experimental source: strains ATCC 43181 and ATCC 44755
A; Experimental source: strains ATCC 43181 and ATCC 44755
A; Experimental source: strains ATCC 43181
A; Indoh, T: Murakami, T: Tsuzuki, K: Yokosawa, N
A; Gen. Microbiol. 137, 519-525, 1991
A; Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E tox
A; Reference number: S16145; MUID: 91237316; PMID: 2033376
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A,Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the A,Reference number: A60027; MUID:90344918; PMID:2116911
A,Accession: A60027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       botulinum neurotoxin type E precursor - Clostridium butyricum
C;Species: Clostridium butyricum
C;Dates: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
C;Accession: JH0256; S16145
R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem Biophys. Res. Commun. 183, 1992
A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum the A;Reference number: JH0256; MUID:92181428; PMID:1543481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.1%; Score 497.5; DB 268.1%; Pred. No. 6.1e-37;
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Matches 94; Conservative 21; Mismatches
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A,Molecule type: DNA
A,Residues: 1-229,'M',231-252 <FUJ>
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hes 93; Conserv
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C;Superfamily: tetanus toxin
C;Superfamily: tetanus toxin
C;Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot
F;2-444/Product: bontoxilysin A light chain #status experimental <HGT>
F;45-1296/Product: bontoxilysin A heavy chain #status experimental <HVY>
F;223, 227/Binding site: zinc (His) #status predicted
F;224/Active site: Glu #status predicted
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A;Ross-references: UNIPROT:Q45894; UNIPARC:UPI000016EA88; EMBL:X73423; NID:g507070; PID
C;Superfamily: tetamus toxin
C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate.
                                                                                                                                                                                                                                                                                                                                                    Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
                                                                                                                                                                                         E.; Suedhof, T.C.; Jahn, R.;
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C;Species: Clostridium botulinum
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40645
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of the light chain of botulinum neurotoxin type
                                                                                                                                                 A;Cross-references: UNIPARC:UP10000173659
R;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, J. Biol. Chem. 269, 1677-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
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A;Title: Sequence of the gene coding for the neurotoxin A;Reference number: I40645; MUID:94143603; PMID:8310180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.9%; Score 440.5; DB 1;
57.6%; Pred. No. 9.3e-32;
tive 26; Mismatches 30;
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      : Partial sequence or since number: A27000
                                                                                                 Molecule type: protein ;Residues: 2-47 <DAS2>
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Matches 82; Conserv
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Best Local Similarity
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                                                                   Accession: A27000
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A; Residues: 1-1296 <BIN>
A; Cross-references: UNIPROT: P10845; UNIPARC: UPI0000001386; GB: M30196; NID: g144864; PIDN:
A; Experimental Bource: Strain 62A, Subtype A
B; Experimental Bource: Strain 62A, Subtype A
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
Biochem. 189, 73-81, 1990
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin
A; Reference number: S09492; MUID: 90235864; PMID: 2185020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPARC:UPI0000173655; EMBL:D67030; DDBJ:D50421; NID:g2160224
Betley, M.J.; Somers, E.; DasGupta, B.R.
ochem. Biophys. Res. Commun. 162, 1388-1395, 1989
Title: Characterization of botulinum type A neurotoxin gene: delineation of the N-term
Reference number: A33401; MUID:89350959; PMID:2669749
                                                                                                                                                                                                                                                                                                                                                                                   Dentoxilysin (BC 3.4.24.69) A precursor - Clostridium botulinum
N.Alternate names: botulinum neurotoxin type A
C.Species: Clostridium, botulinum
C.Species: Clostridium, botulinum
C.Sacession: A35294, S09492, S68220, A33401, A53884, A60025; A27000
R.Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
A. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other A;Reference number: A35294; MUID:90264400; PMID:2160960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1,'O',3-26,'V',28-1296 <THO>
A;Cross-references: UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID
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Gimenez, J.A.; DasGupta, B.R.
Protein Chem. 12, 351-363, 1993
Title: Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, an Reference number: A53884; MUID:94000342; PMID:8397793
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FBBS Lett. 376, 41-44, 1995
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A;Reference number: S67988; MUID:96096783; PMID:8521962
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                                                                                GCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: protein
Residues: 867-880;1148-1217,'Y',1219 <GIM>
Cross-references: UNIPARC:UP100000BBB24; UNIPARC:UP10000173656
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Residues: 2-6;445-453,'X',455-457 <DAS1>
Cross-references: UNIPARC:UP10000173657; UNIPARC:UP10000173658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Botulinum neurotoxin type A: sequence of amino Reference number: A60025; MUID:91120847; PMID:2126206
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NNFINRRTDSTLSINNIR 1112
                                                                                                                                                                        DKSITQNS-NFLNINQQR 138
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lochemistry 26, 4162, 1987
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Molecule type: DNA
Residues: 1-12 <FUJ>
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Residues: 1-35 <BET>
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48940; S48105; S21575; A42871; S07155; S08562; S07128; S08573; S08574
C;Accession: A.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Appl. Environ. Microbiol. 58, 2345-2354, 1992
A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the typ
A;Reference number: A48940; MUID:92384550; PMID:1514783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: type B, Danish
A;Note: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this publics
R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific ic
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Biochimie 70, 811-817, 1988
A;Title: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with A;Reference number: 807155; MUID:89000987; PMID:3139097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;MOlecule type: DNA
A;Residues: 1-1291 <WHE>
A;Cross-references: UNIPROT:P10844; UNIPARC:UP1000016EA76; GB:M81186; NID:G144734; PIDN
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A; Meddues: 36-217, (%', 219-224, 'S', 226-246 <8ZA>
A; Readdues: 36-217, (%', 219-224, 'S', 226-246 <8ZA>
A; Cross-references: UNIPARC: UPIO00016EA79; EMBL: Z11934; NID: 940383; PIDN: CAA77991.1; Pl
B; Kurazono, H.; Mochida, S.; Binz, T.; Eisel, U.; Quanz, M.; Grebenstein, O.; Wernars, U. Biol. Chem. 267, 14721.14729, 1992.
A; Title: Minimal essential domains specifying toxicity of the light chains of tetanus the A; Reference number: A42871; MUID: 92340509; PMID: 1634516
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A;Residues: 634-994 <CAM>
A;Residues: 634-994 <CAM>
A;Cross-references: UNIPARC:UPI000016EA7A; EMBL:X70817; NID:9407782; PIDN:CAAS0148.1;
A;Cross-references: UniPARC:UPI000016EA7A; EMBL:X70817; NID:9407782; PIDN:CAAS0148.1;
                                                                                                                                                                                                                                                                                                   A;Experimental source: proteolytic type B, strain NCTC 7273
R;Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
submitted to the EMBL Data Library, April 1992
A;Description: Partial amino acid sequence of botulinum neurotoxin type B and A;Reference number: S21575
A;Accession: S21575
                                                                                                                                                                                                                                          2 FNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV
                                                                                                                                                                                                                                                                                                                                                                                                                GCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNL--
                                                                              Length 1291;
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A,Note: sequence extracted from NCBI backbone (NCBIP:109365)
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                                                                         38.9%; Score 296; DB 2;
.larity 39.9%; Pred. No. 1.1e-18;
Conservative 29; Mismatches 44
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F;231/Active site: Glu #status predicted
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A, Molecule type: protein
A, Residues: 2-29,'M', 31-45 < DAS>
                                  Query Match
Best Local Similarity
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Rihttson, R.A.; Callina, W.D.; Bast, A.K.; Thompson, D.E.
Curr. Microbiol. 28, 101-110, 1994

A.Accession: 140631, MUID:94122659, PMID:7764370

A.Accession: 140631, MUID:94122659, PMID:7764370

A.Accession: 140631, MUID:94122659, PMID:7764370

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A.Accession: 140631, MUID:94103372, PMID:840864, MUID:9410480

A.Accession: 140631, MUID:94103372, PMID:840864, MUID:9410400000BABE, PMID:840864, MUID:9410400000BABE, PMID:840864, MUID:9410400000BABE, PMID:840864, MUID:9410400000BABE, PMID:84087780, PIDN:CAA50145.1, PIA:870810 PMID:840864, MUID:9410400000BABE, PMID:8408707780, PIDN:CAA50150.1, PIA:870810 PMID:840864, MUID:8407780, PIDN:CAA50150.1, PIA:870810 PMID:840864, MUID:8407780, PIDN:CAA50150.1, PIA:870810 PMID:860810 PMID:840864, MUID:8407780, PIDN:CAA50150.1, PIA:870810 PMID:860810 PMID:840866, PMID:840866, PMID:8407780, PIDN:CAA50150.1, PIA:87080 PDN:A7080 PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:840866, PMID:84086
                                                                                                            neurotoxin - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: O7-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: 839791
R;Campbell, K; Collins, M.D.; Bast, A.K.
Biochim: Biochiw: Acta 1216, 487-491, 1993
A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium a A;Reference number: S39791; MUID:94092745; PMID:8268233
A;Accession: S39791
A;Accession: S39791
A;Accession: S3791
A;Accession: S3797
A;Accession: S3797
A;Accession: S3791
A;Catus: Drellininary
A;Accession: S3797
A;Costarus: Drellininary
A;Costarus: Drellininary
A;Costarus: Drellininary
A;Cross-references: UNIPARC:UPI0000176706; EMBL:X74162; NID:g441275; PIDN:CAA52275.1; PI
C;Acywords: neurotoxin
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49.6%; Pred. No. 1e-18;
live 22; Mismatches 36;
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A,Molecule type: protein
A,Residues: 442-463, R',465-467 <DA2>
A,Cross-references: UNIPARC:UP10000173650
R,Schnidt, J.J., Sathyamoorthy, V: DasGupta, B.R.
Arch. Biochem. Biophys. 238, 544-548, 1985

Cross-references: UNIPARC:UPI0000173650

Molecule type: protein Residues: 442-459 <SCH3> Cross-references: UNIPARC:UP10000173652

atus: preliminary

coss-references: UNIPARC: UPI0000173652

slecule type: protein sidues: 2-17 <SCH2>

atus: preliminary

ross-references: UNIPARC:UPI0000173652

Molecule type: protein Residues: 2-16 <SCH1> ratus; preliminary

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tentoxilysin (BC 3.4.24.68) precursor - Clostridium tetani
NiAlternate names: tetanus neurotoxin
C;Species: Clostridium tetani
C;Species: Clostridium tetani
C;Accession: A25689; A25757; A25184; B22194; A60759; S69348; S09364
C;Accession: A25689; A25757; A25184; B22194; A60759; S69348; S09364
R;Eisel, U; Jarausch, W; Goretzki, K; Henschen, A; Engels, J; Weller, U; Hudel, M.
EMBO J. 5, 2495-2502, 1986
A;Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botu
A;Reference number: A25689; MUID:87053814; PMID:3536478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT: P04958; UNIPARC: UPI000003617E; GB:X04436; NID:940769; PIDN:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-1315 <FAI>
Cross-references: UNIPARC:UP1000003617E; GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G. J. Immunol. 142, 394-402, 1989
J. Immunol. 142, 394-402, 1989
A;Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A;Reference number: US0098; MUID:89093918; PMID:2463305
A;Contents: annotation; epitope region
R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.F.
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A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyi
A;Reference number: S27125; MUID:93063293; PMID:1331807
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Residues: 743-1315 <FA2>
Cross-references: UNIPARC:UPI0000156CFA; GB:M12739; NID:9144920; PIDN:AAA23282.1; PID
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Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment; Reference number: A25194; MUID:86085672; PMID:3510187
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                                                                                                     Length 1276;
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;Molecule type: protein
;Crose-references: UNIPARC:UPI000017364D
;Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe,
nfect. Immun. 57, 3588-3593, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fairweather, N.F.; Lyness, V.A. coleic Acids Res. 14, 7809-7812, 1986
Title: The complete nucleotide sequence of tetanus toxin. Reference number: A25757; MUID:87040747; PMID:3774547
Accession: A25757
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                                                                                                     DB 2;
                                                                                                 32.3%; Score 245.5; DB 2
35.0%; Pred. No. 4.2e-14;
tive 33; Mismatches 55.
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Residues: 461-475 <MAT>
Cross-references: UNIPARC:UP1000017364B
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                                                                                                                                                                                    Conservative
C; Superfamily: tetanus toxin
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Residues: 1-1315 <EIS>
                                                                                                             Query Match
Best Local Similarity
Matches 48; Conserv
                                     C; Keywords: neurotoxin
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C,Accession: S11455
E,Binz, T.; Kurazono, H.; Popoff, M.R.; Eklund, M.W.; Sakaguchi, G.; Kozaki, S.; Krieglis
Nucleic Acids Res. 18, 5556, 1990
A,Title: Nucleotide sequence of the gene encoding Clostridium botulinum neurotoxin type
A,Reference number: S11455; MUID:91016853; PMID:2216736
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A;Cross-references: UNIPROT:P19321; UNIPARC:UPI0000126B83; EMBL:X54254; NID:940395; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R ature 359, 832-835, 1992
Fute: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt, Reference number: S27125; MUID:93063293; PMID:1331807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contents: annotation
Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: annotation c; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic C; Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic C; Genetics: bott/b
A; Gene: bont/b
C; Function: A; Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2 A; Description: catalyzes hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc; Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc; F; 2441/Product: bontoxilysin B light chain #status experimental <LGHT> F; 2442-1291/Product: bontoxilysin B heavy chain #status experimental <LHVY> F; 230, 234/Binding site: zinc (His) #status predicted
F; 231/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                Title: Partial amino acid sequences of botulinum neurotoxins types Reference number: $07128; MUID:85197963; PMID:3888113
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botulinum neurotoxin type D - Clostridium botulinum

Species: Clostridium botulinum

A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-1276 <BIN>

A, Accession: S11455

KNSYIKLKKDSPVGEILTRSKYNQNSKYIN 1135 119 -----TRTDKSI------TQNSNFLN 133

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Appl. Environ. Microbiol. 57, 1168-1172, 1991
A;Title: Cloning of the structural gene for Clostridium botulinum type C-1 toxin and A;Reference number: A49777; MUID:91282468; PMID:2059039
A;Referus: prelliminary
A;Scatus: prelliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-607 <TS3>
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31.4%; Score 239; DB 2; L. Best Local Similarity 37.0%; Pred. No. 1.7e-13; Marches 54; Conservative 25; Mismatches 57;
                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI000017670A; GB:D90210
C;Superfamily: tetanus toxin
C;Keywords: neurotoxin
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Matches 54; Conserv
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C/Species: Clostridium botulinum
C/Species: Clostridium botulinum
C/Species: Clostridium botulinum
C/Species: Clostridium botulinum
C/Species: D-Mar-1994 #sequence revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: S11291; A35396; $22166; A49777
R/Hauser, D.; Eklund, M.W.; Kurazono, H.; Binz, T.; Niemann, H.; Gill, D.M.; Boquet, P.;
Nucleic Acids Res. 18, 4924, 1990
A/Ttele: Nucleotide sequence of Clostridium botulinum C1 neurotoxin.
A/Reference number: S11291; MUID:90370487; PMID:2204031
A/Reference number: S11291; MUID:90370487; PMID:2204031
A/Residues: 1-84, P.; 86-1291 c-HAU-
A/Residues: 1-84, P.; 86-1291 c-HAU-
A/Residues: 1-84, P.; 86-1291 c-HAU-
A/Residues: 1-84, P.; Fulii, N.; Teuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Takeshi, K.
Biochem: Biophys. Res. Commun. 171, 1304-1311, 1300
A/Reference number: A35396; MUID:91024998; PMID:2222445
A/Accession: A35396
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                                                                                                                                                                                             A; Molecule type: protein
A; Mesidues: 2-31 < DEF.
A; Residues: 2-31 < DEF.
A; Residues: 2-31 < DEF.
A; Residues: 2-31 < DEF.
C; Comment: The Bource of this protein was an extrachromosomal plasmid.
C; Comment: The precursor is cleaved by endogenous proteinase activity to form light (fradual chains are not toxic when separated). The amino end of the heavy chain (fragment B)
C; Comment: Fragment E forms ion channels in a lipid bilayer. Fragment C binds to ganglid C; Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
    Ride Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C. Eur. J. Biochem. 229, 61-69, 1995
A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.
A;Reference number: S69348; MUID:95262688; PMID:7744050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synap C; Superfamily: tetanus toxin C; Superfamily: tetanus toxin C; Reywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc C; Reywords: hydrolase; metalloproteinase; neurotoxin; fragment A) #status predicted TTL: P: 45-457/Product: tentoxylysin heavy chain (fragment B) E) #status predicted TTL: F: 461-664/Domain: channel forming (fragment B) #status predicted TXB> F: 865-1315/Domain: ganglioside binding (fragment C) #status predicted TXC> F: 233,237/Binding site: zinc (His) #status predicted
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A;Cross-references: UNIFARC:UPI00000B3F60; EMBL:X62389; NID:g558175; PIDN:CAA44263.1; P. R;Kimura, K.; Fujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Oguma, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.6%; Score 240.5; DB 1; Best Local Similarity 42.0%; Pred. No. 1.2e-13; Matches 47; Conservative 22; Mismatches 42;
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A;Accession: S22166
A;Status: preliminary
A;Molecule type: DNA
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and its associated non-toxic py
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R.Hauser, D.; Eklund, M.W.; Boquet, P.; Popoff, M.R.
R.Hauser, D.; Eklund, M.W.; Boquet, P.; Popoff, M.R.
Mol. Gen. Genet. 243, 531-640, 1994
A.?Title: Organization of the botulinum neurotoxin C1 gene and its associated non-toxic A; Reference number: S46426; MUID:94331293; PMID:8028579
A.Accession: S46431
A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-1291 cHAU>
A.Residues: 1-1291 cHAU>
A.Residues: UNIPROT:Q93HT3; UNIPARC:UP100000B3F60; EMBL:X72793; NID:9516171; B.
A.Cross-references: UNIPROT:Q93HT3; UNIPARC:UP10000B3F60; EMBL:X72793; NID:9516171; B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: strain C 468
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Superfamily: tetanus toxin
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                                                                                                                                                         1052 KIPDTGLITSDSDNINMMIRDFYIFAKELDGKDINILFNSLQYTNVVKDYMGNDLRYNKE 1111
                                                                                                                                                                                                                                                       GCNDTRYV------GIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKR 112
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                                                                                                                  2 FNYTQMISISDYINKWIPVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV 61
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C;Species: Clostridium botulinum phage 1C
A;Vaiiety: strain C 468
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
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botulinum neurotoxin type Dsa precursor - Clostridium botulinum phage d-sA
C;Species: Clostridium botulinum phage d-sA
A;Note: host Clostridium botulinum type D (strain South Africa)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
                                                                    Gaps
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Length 1291;
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                                                            Indels
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PIDA

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R.Fujii, N.; Kimura, K.; Yokosawa, N.; Yashiki, T.; Tsuzuki, K.; Oguma, K. J. Gen. Microbiol. 139, 79-86, 1993
A;Title: The complete nucleotide sequence of the gene encoding the nontoxic component of A;Reference number: A47708; MUID:93195515; PMID:8450310
A;Contents: type E, Mashike
A;Accession: A47708
                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-1285 4003>
A; Residues: 1-1285 4003>
A; Residues: 1-1285 4003>
A; Residues: 1-1285 4003>
A; Crose-references: UNIPARC: UPI00000B54BA; EMBL: D38442; NID: g1374775; PIDN: BAA07477.1; F
C; Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neu
a disulfide bond. The heavy chain mediates the binding of toxin to the presynaptic membr
C; Superfamily: tetanus toxin
C; Superfamily: tetanus toxin
C; Reywords: disulfide bond; neurotoxin; transmembrane protein
F;1-447/Product: botulinum neurotoxin type Dsa light chain #status predicted <MATI>
F;448-1285/Product: botulinum neurotoxin type Dsa heavy chain #status predicted <MATI>
R;Moriishi, K.; Koura, M.; Abe, N.; Fujii, N.; Fujinaga, Y.; Inoue, K.; Ogumad, K. Biochim. Biophys. Acta 1307, 123-126, 1996
A;Title: Mosaic structures of neurotoxins produced from Clostridium botulinum types C an A;Reference number: S70582; MUID:96283801; PMID:8679691
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A; Residues: 1-1162 <FUJ>
A; Cross-references: UNIPARC:UP1000017ACE7
A; Note: sequence extracted from NCBI backbone (NCBIN:127249, NCBIP:127250)
C; Superfamily: tetanus toxin
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045851_9CLOT
BXF_CLOBO
BXE_CLOBO
054A79_CLOBO
BXE_CLOBO
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093ht3 clostridium 045967 clostridium 060798 clostridium 060797 clostridium 033871 clostridium 033871 clostridium 045888 clostridium 045888 clostridium 060277 clostridium 060277 clostridium 060366 clostridium 060366 clostridium 060366 clostridium 060366 clostridium 060366 clostridium 060366 clostridium 060366 clostridium 060366 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostridium 060360 clostr
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Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, X81714; CAA57358-1; -; Genomic_DNA.
EMBL, L15466; AAA21210.1; -; Genomic_DNA.
EMBL, L15466; AAA21210.1; -; Genomic_DNA.
EMBL, L154894; 1E1H.
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STRAIN-NCTC 10281;
HUESON R.-N. COllins M.D.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
BONT/F (Neurotoxin type F);
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Neurotoxin.
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Q57236; Q45863;
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BXF CLOBO
P30996;
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BXF_CLOBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Santos-Buelga J., Collins M.D., East A.K.; "Characterization of the genes encoding the Botulinum neurotoxin complex in a strain of clostridium botulinum producing type B & F neurotoxins.";
                                                                                                                                                                                                                                                                              Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CDC 3281; PubMed=9767710; DOI=10.1007/s002849900384; MEDLINE=98440323; PubMed=9767710; DOI=10.1007/s002849900384;
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RGO; GO:0016021; C:integral to membrane; IEA.

RGO; GO:0009405; P:pathospetidase activity; IEA.

RGO; GO:0009405; P:pathospenseis; IEA.

RGO; GO:0009405; P:pathospenseis; IEA.

RGO; GO:0009508; P:pathospenseis; IEA.

RILE-Pro; IPR001591; Botulinum.

RILE-Pro; IPR001035; Peptidase_M27.

R PEANYE; PR00760; BONYOXILYSIN.

R PROBITE; PR00760; BONYOXILYSIN.

R PROBITE; PS001963; BOTULINUM; 1.

R PROSITE; PS001963; BOTULINUM; 1.

R PROSITE; PS001963; AINT PROTESE; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Santos-Buelga J.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y13631; CAA73972.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
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Last sequence update)
Last annotation update)
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85.0%; Pred. No. 6.7e-49;
ive 9; Mismatches 12;
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                                                                                                                               PRT; 1280 AA
1115 KDKYITRNSGILNINQQRGV 1134
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01-MAY-1999 (TEMBLrel. 26,
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Q45851;
Q15851;
Q1-NOV-1996 (TEMBLEH: 01,
Q1-NOV-1996 (TEMBLEH: 01,
NOT-094 (TEMBLEH: 26,
Neurotoxin type F.
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Best Local Similarity 85.0
Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1491;
                                                                                                                                                                                                                                        protein.
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                                                                                    RESULT 2
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61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                  MUCLEOTIDE SEQUENCE.

MEDLINE=93252228; PubMed=8486245; DOI=10.1016/0378-1097(93)90581-L;
Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.,
Richardson P.T.;
"Nucleotide sequence of the gene coding for Clostridium barati type Ineuroticxin: comparison with other clostridial neurotoxins.";
FEMS Microbiol. Lett. 108:175-182(1993).
PIR: $33411; $33411.
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STRAIN=TYPE F / ATCC 23387;
MEDLINE=93012902; PubMed=1398040; DOI=10.1016/0378-1097(92)90408-G;
East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A.,
Thompson D.E.;
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Clostridium baratii.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BONT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.7%; Score 622; DB 2; Length 1268; 79.0%; Pred. No. 5.5e-48; ive 16; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1268 AA; 145512 MW; 963040091AC15ED2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q45894; 1E1H.

MEROPS; M27.002; -...
GO; GO:0016021; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR000505; Peptidase M27.
InterPro; IPR006025; Pepti M. Zn. BS.
Pfam; PF01742; Peptidase M27; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEMS Microbiol. Lett. 75:225-230(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TDKSITQNSNFLNINQQRGVYQK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botulinum neurotoxin F heavy chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00760; BONTOXILYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
NUCLEOTIDE SEQUENCE OF 1-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 79.0%;
Matches 113; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium botulinum.
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-!- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 58-Gln-|-Lys-59 bond of synaptobrevins-1 and -2.

-!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

-!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).

-!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                 MEDLINE=94013372; PubMed=8408542; Campbell K.D., Collins M.D., East A.K.; Mence probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                       East A.K., Collins M.D.; "Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteolytic Clostridium botulinum type F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLUIAR LOCATION: Secreted.
MISCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF07953; Toxin_R_bind_N; 1.
Pfam; PF07952; Toxin_trans; 1.
PRINTS; PR00766; BONTFOXILYSIN.
PRODOM; PD001963; BOLUlinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulinum neurotoxin F light chain.
Botulinum neurotoxin F heavy chain.
By similarity.
Zinc (catalytic) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formation and toxin binding, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M92906; AAA23263.1; -; Genomic_DNA.
EMBL; S73876; AAC60475.1; -; Genomic_DNA.
EMBL; X70820; CAA5015.1.1; -; Genomic_DNA.
EMBL; X70816; CAA50147.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006025; Pept M_Zn_BS.
InterPro; IPR000395; Peptidase M27.
InterPro; IPR012928; Toxin_recpt_bd_
InterPro; IPR012500; Toxin_trans.
                                                                                                                                                                                                                                                                                                                                     MEDLINE=94230352; PubMed=8175689;
STRAIN=Type F / Hobbs FT10;
MEDLINE=94297488; PubMed=7764998;
                                                                                                                         Curr. Microbiol. 29:69-77(1994).
                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF.634-1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR011591; Botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'oxin, Transmembrane; Zinc.
                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
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PIR; S48109; S48109.
HSSP; Q45894; 1E1H.
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228
227
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VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92174922; PubMed=1541280; Whelan S.M.; Blmore M.J.; Back and M.J.; Bedsworth N.J.; Atkinson T.; Minton N.P.; "The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                                                                                                                                         1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 4375)."; Biochem. Biophys. Res. Commun. 183:107-113(1992).
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Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                                                                                                                                                                                                                                                                                  BXE CLOBU

000496, Q45862;

01-JUL-1993 (Rel. 26, Last sequence update)

01-JUL-1993 (Rel. 26, Last annotation update)

13-SEP-2005 (Rel. 48, Last annotation update)

Botulinum neurotoxin type E precursor (EC 34.24.69) (BONT/E)

Botulinum neurotoxin E light chain;

----ilvain E) (Contains: Botulinum neurotoxin E light chain;

----ilvain E) (Contains: Asavy chain).
              Interchain (between light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Zinc (catalytic) (By similarity)
                                                                                     Length 1274;
                                                                                                                        14; Indels
                                                 146710 MW; 5B99756A7438B921 CRC64;
                                                                                     ; DB 1;
4.5e-47;
                                     (Probable
                                                                                                       Pred. No. 4.5e-10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1250 AA.
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                                                                                       Score 612;
Pred. No. 4
                                     chains)
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                                                                                                                                                                                                                                                                                                                                           1114 KDKYITLNSGILNINQORGV 1133
                                                                                                                                                                                                                                                                                                        TDKSITQNSNFLNINQQRGV 140
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MEDLINE=92181428; PubMed=1543481;
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                                                                                       80.4%;
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                                                                                                                        Matches 116; Conservative
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 231
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                                                       1274 AA;
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                                                                                                           Similarity
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                  DISULFID
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                                                       SEQUENCE
                                                                                          Query Match
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Matches
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J. Meman H.;

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J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

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J. Biol. Chem. 269:1617-1620(1994).

J. Biol. Chem. 269:1617-1620(1994).

J. Chem. 269:1617-1620(1994).

J. Milliphies neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 180-Arg-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-11e-|-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **STRAIN=TYPE B / Hazen 36208;
MEDLINE=94013372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxin gene and
specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                        MEDLINE=94663091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schlavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Benfenati F., Wilson M.C., Montecucco C.; Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds "; FEBS Lett. 335:99-103(1993).
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EMBL; X62683; CAA44558.1; -; Genomic_DNA.

EMBL; X70815; CAA50146.1; -; Genomic_DNA.

PIR; S08575; S08575.

PIR; S11778; S21178.

PDB; 1T3A; X-ray; A/B=1-421.
                                                                                                                                                                                                                                                                                                                     IDENTIFICATION OF SUBSTRATE.
                                                                                                                                                                           IDENTIFICATION OF SUBSTRATE
Biochimie 72:213-217(1990)
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Tsukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa T.,
Nakamura S., Karasawa T., Kozaki S.;
Sequence of the botulinum neurotoxin type E.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
         By similarity.
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Interchain (between light and heavy chains) (Probable).
R - 9 (in Ref. 2).
C -> S (in Ref. 2) and 3).
I -> L (in Ref. 2 and 6).
FB -> L (in Ref. 2 and 6).
FB -> LQ (in Ref. 2 and 6).
FB -> A (in Ref. 2 and 6).
R -> A (in Ref. 2 and 6).
R -> A (in Ref. 2 and 6).
N -> NN (in Ref. 2 and 6).
N -> NN (in Ref. 2 and 6).
N -> NN (in Ref. 2 and 6).
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Botulinum neurotoxin E heavy chain.
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                                                                                                                                                                                                                                                                          Length 1250;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Botulinum neurotoxin type E.
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                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                      / Match 65.4%; Score 497.5; DB 1
Local Similarity 68.1%; Pred. No. 1.4e-36;
hes 94; Conservative 21; Mismatches 22
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1094 NNFIDRRKDSTLSINNIR 1111
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966 96
1194 119
1250 AA;
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NUCLEOTIDE SEQUENCE.
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ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         i-FUNCTION: Boculinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yashiki T., Oguma K.; "I compare the S'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340."; ". Gen. Microbiol. 137:519-525 (1991).
                                                                                                                                                                                                                                                                                    STRAIN=BL6340;
MEDLINE=91237316; PubMed=2033376;
Pujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N.,
                                                                                                                                                                            MEDLINE=SIZE 43181, and ATCC 43755;
MEDLINE=92181428; PubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium bype E (strain Beluga) and Clostridium buryricum (strains ATCC 43181 and ATCC 43755).";
                                                                                                             Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
(Bontoxilyain E) (Contains: Botulinum neurotoxin E light chain;
Botulinum neurotoxin E heavy chain).
                                                                                                                                                                                                                                                                                                                                                                                                 Gimenez J., Foley J., Dasgupta B.R.;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.";
PASEB J. 2.A1750-A1750(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endopeptidase.
CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 183:107-113(1992)
                       PRT; 1250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X62088; CAA43998.1; -; Genomic_DNA.
EMBL; X53180; CAA37321.1; -; Genomic_DNA.
PIR; JH0256; JH0256.
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR000395; Peptidase M27.
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                       STANDARD;
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InterPro; IPR006025;
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                                                                                                                                                NCBI_TaxID=1492;
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                      BXE CLOBU
P30995;
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62 GCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRT 121
Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF01742; Peptidase MZ7; 1.
Pfam; PF07953; Toxin_R bInd_N: 1.
Pfam; PF07952; Toxin_R Lians; 1.
PRINTS; PR00760; BONTOXILISIN.
PRODOM; PD01963; Botulinum; 1.
PROSITE; PS00442; ZINC_PR0TEASE; 1.
Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
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TBUKamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa T.,
Nakamura S., Karasawa T., Kozaki S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB088207; BAC05434.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                             212 212 By similarity.
211 211 Zinc (catalytic) (By similarity).
215 215 Zinc (catalytic) (By similarity).
411 425 Interchain (between light and heavy chains) (Probable).
229 229 K -> M (in Ref. 2).
1250 AA, 143266 MW; 8171B5B2C2312857 CRC64;
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                                                                                                                                                                                                                                                          Botulinum neurotoxin E light chain.
Botulinum neurotoxin E heavy chain.
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PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1252 AA; 143510 MW; 41B633BB744D3B41 CRC64;
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GO:0008237; F:metallopeptidase activity; IEA.
GO:0009405; P:pathogenesis; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
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Last annotation update)
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InterPro, IPR000395; Peptidase M27.
InterPro, IPR006025; Peptidase M27.
BS.
Pfam; PP01742; Peptidase M27; I.
PRINTS; PR00760; BONTOXILYSIN.
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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QBKZM3 CLOBU
ID QĒKZM3_CLOBU PRELIMINARY;
AC QBKZM3;
AC QBKZM3;
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Matches 93; Conservative
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1250
212
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WICHELDINE SEQUENCE.

WICHELDINE SEQUENCE.

WICHELDINE SEQUENCE.

WEDLINE=2009829; PubMed=1105594;

DOI=10.1128/AERG.

Wang X., Meegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,

Wang X., Meegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y.,

A wandkawa K., Oguma K., Sakaguchi Y., Nakamura S.;

"Genetic analysis of type E botulinum toxin-producing Clostridium
butyricum strains.";

"Genetic analysis of type E botulinum toxin-producing Clostridium
butyricum strains.";

"Genetic analysis of type E botulinum toxin-producing Clostridium
butyricum strains.";

"Genetic analysis of type E botulinum toxin-producing Clostridium
butyricum strains.";

"Genetic analysis of type E botulinum.

R Appl. Environ. Microbiol. 66:4922-4997(2000).

R RSEP, GASBA6; Bahl.

GO, GO:0008237; Fametallopeptidase activity; IEA.

GO, GO:0008237; Fimetallopeptidase activity; IEA.

GO, GO:0008237; Fimetallopeptidase and peptidolysis; IEA.

R DO: GO:0008205; Peptidase M27.

InterPro: IPR001095; Peptidase M27.

InterPro: IPR001095; Peptidase M27.

R PRINTS; PR00142; EURC FROTESES; UNKNOWN 1.

PRODOM; PROSITE; PS00142; ZUC PROTESES; UNKNOWN 1.

R PROSITE; PS00142; ZUC PROTESES; UNKNOWN 1.
                                                                                                      2 FNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV 61
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Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Query Match
Best Local Similarity 67.4%; Pred. No. 2.1e-36;
Matches 93; Conservative 23; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type E botulinum toxin.
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Q9FAR6;
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Matches 93; Conserva
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974 VFKYGNANGISDYINKWIFVTITNDRLGDSKLYINGHLIDQKSILNLGNIHVSDNILFKI 1033
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A MEDLIA = 2009423; Windred = 11039294;

A YamaKawa K., Garma W.; Karasawa T.; Kozaki S.; Tsukamoto K., Gyobu Y.,

A YamaKawa K., Oguma K.; Sakaguchi Y., Nakamura S.;

T "Genetic analysis of type E botulinum toxin-producing Clostridium

Dutyricum strains.";

T Appl. Environ. Microbiol. 66:4992-4997 (2000).

R EMBL; AB037714; BAB03512.1; -; Genomic_DNA.

R EMBL; AB037706; BAB03512.1; -; Genomic_DNA.

R EMBL; AB037710; BAB03518.1; -; Genomic_DNA.

R EMBL; AB037710; BAB03518.1; -; Genomic_DNA.

R EMBL; AB037711; BAB03518.1; -; Genomic_DNA.

R EMBL; AB037711; BAB03519.1; -; Genomic_DNA.

R EMBL; AB037711; BAB03519.1; -; Genomic_DNA.

R EMBL; AB037711; BAB03519.1; -; Genomic_DNA.

R EMBL; AB037711; BAB03519.1; -; Genomic_DNA.

R EMBL; AB037709; BAB03519.1; -; Genomic_DNA.

R EMBL; AB037709; BAB03519.1; -; Genomic_DNA.

R EMBL; AB037709; BAB03519.1; -; Genomic_DNA.

R EMBL; AB037709; BAB03519.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLECTIDE SEQUENCE.
STRAIN=LCL 095, LCL 155, KZ 1899, KZ 1897, KZ 1898, KZ 1886, KZ 1887,
KZ 1889, KZ 1891, and LCL 063;
MEDLINE=20509829; PubMed=11055954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                  Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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2021F4E427070296 CRC64;
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GG: GO: 0005405; F:peptidase activity; IEA.

GG: GO: 0005405; F:peptidase is IEA.

GG: GO: 0005680; F:petidase is IEA.

GG: GO: 0005580; F:petidase is IEA.

InterPro; IPR01591; Botulium.

R InterPro; IPR015929; Foxtul reage.

R InterPro; IPR012500; Toxin recpt bd.N.

R Pfam; PP07951; Toxin Lrans.

R Pfam; PP07951; Toxin Lrans.

R Pfam; PP07952; Toxin Lrans.

R Pfam; PP07952; Toxin Lrans.

R Pfam; PR07953; Toxin Lrans.

R Pfam; PR07953; Toxin Lrans.

R Pfam; PR07953; Ioxin Lrans.

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                                                                                                                                      Last sequence update)
Last annotation update)
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ilarity 66.9%; Pred. No. 9.1e-36;
Conservative 22; Mismatches 23;
    PRT; 1251 AA
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                                                                               01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-FBE-2005 (TrEMBLrel. 29,
Type B botulinum toxin.
Q9K395_CLOBU PRELIMINARY;
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Best Local Similarity
Matches 93; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1492;
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HSSP; Q45894;
SMR; Q9K395;
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BXA1_CLOBO
ID BXA1_CLOBO
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Dasgupta B.R., Foley J., Niece R.; "Partial sequence of the light chain of botulinum neurotoxin type A."; Biochemistry 26:4162-4162(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Betley M.J., Somers E., Dasgupta B.R.; "Characterization of botulinum type A neurotoxin gene: delineation of
                                                                                                                                                                                                                                                                                                                                                                       Thompson D.E., Brehm J.K., Oultram J.D., Swinfield T.-J., Shone C.C., Atkinson T., Melling J., Minton N.P., The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Past A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic Clostridium botulinum types A. B. and F. evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99264400; PubMed-2160960;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
The complete sequence of bottulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
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                     01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
13-SRP-2005 (Rel. 48, Last annotation update)
13-SRP-2005 (Rel. 48)
13-SRP-2005 (Rel. 48)
14-SRP-2005 (Rel. 48)
15-SRP-2005 (Rel. 48)
16-SRP-2005 (Rel. 48)
                                                                                                                                                                                                         Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the N-terminal encoding region.";
Biochem. Biophys. Res. Commun. 162:1388-1395(1989).
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                                                                                                                                          chain; Botulinum neurotoxin A heavy-chain].
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MEDLINE=97016817; PubMed=8863443;
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                                                                                                                                                                                                                                                                                                                            STRAIN=Type A / NCTC 2916;
MEDLINE=90235864; PubMed=2185020;
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                                                                                                                                                                  Name=botA; Synonyms=atx, bna;
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                                                                                                                                                                                        Clostridium botulinum.
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                                                                                                                                                                                                                                                           NCBI_TaxID=1491;
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                                                                                                                                                                                                                                        Clostridium
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    HARREN BERTA
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FUNCTION: Inhibits acetylcholine release. The botulinum toxin FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-cln-l-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release
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MEDLINE=98455071; PubMed=9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain (H).
SUBCELUULAR LOCATION: Secreted.
PHARMACEUTICAL: Available under the name BOTOX (Allergan) for the
treatment of strabismus and blepharospasm associated with dystonia
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CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

COFACTOR: Binds 1 zinc ion per subunit.

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN SEQUENCE OF 448-482.
MEDLINE=85285016; PubMed=3896784;
Shone C.C., Hambleton P., Melling J.;
Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C., Jahn R., Niemann H.; "Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gimenez J.A., DasGupta B.R.;
"Botulinum trype A neurotoxin digested with pepsin yields 132, 97, 72,
45, 42, and 18 kD fragments.";
J. Protein Chem. 12:351-363(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; "Botteninum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds."; PEBS Lett. 335:99-103(1993).
                                                                                                                                                                 MEDLINE-89024662; PubMed-3178218;
Sathymoorthy V., Dasgupta B.R., Foley J., Niece R.L.;
"Botulinum neurotoxin type A: cleavage of the heavy chain into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS OF GLU-261, PHB-265 AND TYR-365.
MEDLINE=21556941, PubMed=11700044, DOI=10.1006/bbrc.2001.5911;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
"Site-directed mutagenesis identifies active-site residues of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   light chain of botulinum neurotoxin type a.";
Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
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                                                                                                                                                                                                                                                                                                                         Arch. Biochem. Biophys. 266:142-151(1988)
                                                                                                                      PROTEIN SEQUENCE OF 448-474 AND 872-895.
terminus and around the nicking site.";
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                                          Biochimie 72:661-664(1990)
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PRT; 1296 AA

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Q7B8V4 CLOBO PRELIMINARY;
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                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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R InterPro; IPR011591; Botulinum.
R InterPro; IPR000395; Peptidase M27.
R InterPro; IPR00395; Peptidase M27.
R InterPro; IPR012500; Toxin_trans.
R Pfam; PF01742; Peptidase M27; 1.
R Pfam; PF017953; Toxin_trans L Dind. N; 1.
R Pfam; PF007953; Toxin_trans 1.
R PRINTS; RP00760; BONTOXILYSIN.
R PROSTIE; PS00142; ZINC_PROTEASE; 1.
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R PROSTIE; PS00142; ZINC_PROTEASE; 1.
R PROSTI
                                                                                                                                              WWW="http://www.Dotox.com/site/".
DATABASE: NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;
WWW="http://www.expasy.org/spotlight/back_issues/sptlt019.shtml".
and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.
MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A. B. Ci. D. E. F. and G. SIMILARITY: Belongs to the peptidase M27 family.

DATABASE: NAME=BOTOX product information Web site;
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Pred. No. 2.3e-31;
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EMBL; M30196; AAA23262.1; -;
EMBL; X92973; CAA63551.1; -;
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RESULT 12 Q7B8V4\_CLOBO

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MEDLINE=22919384; Pubmed=14557061; DOI=10.1016/S0378-1119(03)00792-3;
Zahang L., Lin W.J., Lit S., Aoki K.R.;
"Complete DNA sequences of the botulinum neurotoxin complex of
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MEDLINE=S4413603; PubMed=8310180, DOI=10.1016/0923-2508(93)90004-L;
MEDLINE=S4413603; PubMed=8310180, DOI=10.1016/0923-2508(93)90004-L;
Willems A., East A.K., Lawson P.A., Collins M.D.;
"Sequence of the gene coding for the neurotoxin of Clostridium
botulinum type A associated with infant botulism: comparison with
other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                                                                                                                                                                 Dineen S.S., Bradshaw M., Johnson B.A.;
"Neurotoxiin gene clusters in Clostridium botulinum type A strains: sequence comparison devolutionary implications.";
Curr. Microbiol. 46:345-352(2003).
                                                                                                                                                                                                                                                                                      STRAIN=Hall A-hyper;
MEDLINE=22617869; PubMed=12732962; DOI=10.1007/800284-002-3851-1;
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28-FFBS-2003 (Rel. 41, Created)
28-FFBS-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
(Boutlinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain].
                                                                                                                                  Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium botulinum type A-Hall (Allergan) strain.";
Gene 315:21-32(2003).
EMBL, F461540; AAW75961.1; -; Genomic_DNA.
EMBL, AF488749; AAQ06331.1; -; Genomic_DNA.
                          Last sequence update)
Last annotation update)
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          Created)
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10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
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                                                                                  BONT/A (Neurotoxin BONT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                  Int. J. Syst. Bacteriol. 46:1105-1112(1996).

-1- FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release
                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity)
SUBCELLULAR LOCATION: Secreted.
                                        MEDLINE=97016817; PubMed=8863443;

East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";
                                                                                                                                                                                                                                                                                                results in flaccid paralysis, with frequent heart or respiratory failure (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1D-structure; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANBOUGS: There are seven antigenically distinct forms botulinum neurotoxin: Types.A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botulinum neurotoxin A light-chain.
Botulinum neurotoxin A heavy-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinc (catalytic) (By similarity).
Linc (catalytic) (By similarity).
Interchain (between light and heav chains) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.7%; Score 423.5; DB 1; Length 1295; 56.9%; Pred. No. 8.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.

My; 5DA04A13D98D6372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR00625; Pept M Zn BS.
InterPro; IPR010395; Pept M Zn BS.
InterPro; IPR012928; Peptidase M27.
InterPro; IPR012928; Toxin_trans.
Pfam; PF01742; Peptidase M27; 1.
Pfam; PF07953; Toxin_R bind_N; 1.
Pfam; PF07953; Toxin_R bind_N; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Potential.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxin; Transmembrane; Zinc.
0 0 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X73423; CAA51824.1; -; Genomic_DNA.
EMBL; X87974; CAA61234.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1E1H; X-ray; A/C=9-249, B/D=250-415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1295 AA; 149280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interPro; IPR011591; Botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222
226
453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; 140645; 140645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; M27.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease;
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61 VGCND-TRYVGIRYPKVPDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
                                                                         VGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith T.J., Iou J., Geren I., Forsyth C., Tsai R., Tepp W.H., Bradshaw M., Johnson B.A., Smith L.A., Marks J.D.; "Sequence variation within botulinum neurotoxin serotypes impacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type A2 botulinum neurotoxin.
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson B.A., Tepp W.H., Bradshaw M., Gilbert R.J., Cook P.E.,
McIntosh B.D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1296 AA; 149410 MW; 6F12E7BF28ED69D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody binding and neutralization.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 25, Last annotation update)
Botulinum neurotoxin type B (Fragment).
Name=boNI/B;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                    PRT; 1296 AA.
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                                                                                                                                                                                                :|:|:||::||
1117 DPNKYVDVN----NIGIRGYMYLK 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RTDKSITQNSNFLNINQQRGVYQK 143
                                                                                                                                                                     120 RIDKSITONSNFLNINQORGVYOK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Q9X708;
                                                                                                                                                                                                                                                                                                                                      Q58GH1_CLOBO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FRI-H1A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FRI-H1A2;
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23; Mismatches

Conservative

Best Local Similarity Matches 82; Conserv

Indels

NCBI\_TaxID=1491;

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62 GCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNL-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 GDIDRIQFIWMKYFSIFNTELSQSNIKEIYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGN 263
                                                                                                                                                                                                                                                                                                                                                                    2 PNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIV 61
                                                                                                                                                                                                                                                                                                Query Match

39.6%; Score 301; DB 2; Length 441;
Best Local Similarity 39.9%; Pred. No. 4.1e-19;
Matches 63; Conservative 30; Mismatches 43; Indels 22; Gaps
                        MUCLEOTIDE SEQUENCE.
MEDLINE=99343691; PubMed=10413679;
MEDLINE=99343691; PubMed=10413679;
Schlavo G.;
Farreros J., Osborne S.L., Montecucco C., Rossetto O.,
Schlavo G.;
"Functional characterisation of tetanus and botulinum neurotoxins
binding domains.";
J. Cell Sci. 112:2715-2724(1999).
EMBL; AJ242628; CAB43706.1; -; Genomic_DNA.
HNSP; P10844; LEFW.
GO; GO:0009405; P:pathogenesis; IEA.
Neurotoxin.
                                                                                                                                                                                                                                 1 1
441 441
441 AA; 52772 MW; 721D0B468E8C95A4 CRC64;
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Search completed: March 2, 2006, 00:46:24 Job time: 73.8376 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein Run on:

March 2, 2006, 00:46:47; Search time 17.7077 Seconds (without alignments) 672.325 Million cell updates/sec

US-08-981-087B-3 761 1 VFNYTQMISISDYINKWIFV......ITQNSNFLNINQQRGVYQKP 144 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 seqs, 82675679 residues Searched: 572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptcdata/1/iaa/6\_COMB.pep:\*
/cgn2\_6/ptcdata/1/iaa/H\_COMB.pep:\*
/cgn2\_6/ptcdata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptcdata/1/iaa/RE\_COMB.pep:\*
/cgn2\_6/ptcdata/1/iaa/RE\_COMB.pep:\* Patents AA Issued Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result No.	Score	Query Match	ouery Match Length DB	DB	ΙD	Description
	440 5	57.9	382		TIS-09-288-326A-9	Sequence 9, Appli
10	440.5	57.9	382	1 (1	US-09-548-409B-9	6
ım	440.5	57.9	438	Н	US-08-480-604A-23	Sequence 23, Appl
4	440.5	57.9	438	Н	US-08-405-496A-23	23
Ŋ	440.5	57.9	438	~	US-08-915-136-23	23
9	440.5	57.9	438	~	US-09-084-517-23	23,
7	440.5	57.9	462	Н	US-08-480-604A-26	56
80	440.5	57.9	462	-	US-08-405-496A-26	26,
6	440.5	57.9	462	~	US-08-915-136-26	26,
10	440.5	57.9	462	7	US-09-084-517-26	
11	440.5	57.9	1296	~	US-08-480-604A-28	28,
12	440.5	57.9	1296	Н	US-08-405-496A-28	28,
13	440.5	57.9	1296	~	US-08-915-136-28	Sequence 28, Appl
14	440.5	57.9	1296	7	US-09-084-517-28	Sequence 28, Appl
15	423.5	55.7	848	7	US-10-360-101-219	Sequence 219, App
16	284.5	37.4	1169	7	US-09-255-829-20	Sequence 20, Appl
17	284.5	37.4	1290	7	US-10-360-101-220	Sequence 220, App
18	240.5	31.6	452	-	US-07-618-312A-2	Sequence 2, Appli
19	240.5	31.6	452	Н	US-07-618-312A-4	Sequence 4, Appli
20	240.5	31.6	452	Н	US-08-280-228-2	Sequence 2, Appli
21	240.5	31.6	452	ч	US-08-280-228-4	4,
22	240.5	31.6	618	Н	US-08-668-381A-5	Ŋ
23	240.5	31.6	853	~	US-08-913-880C-17	17,
24	240.5	31.6	858	~	US-08-913-880C-16	16,
25	240.5	31.6	860	N	US-08-913-880C-15	15,
56		31.6	862	~	US-08-913-880C-14	Sequence 14, Appl
27	240.5	31.6	865	N	US-08-913-880C-13	13,

Sequence 12, Appl Sequence 11, Appl Sequence 10, Appl Sequence 1, Appl Sequence 14679, A Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 52, Appl	Sequence 62, Appl Sequence 21, Appl
US-08-913-880C-12 US-08-913-880C-11 US-08-913-880C-10 US-08-913-880C-1 US-08-110-786A-8 US-08-110-786A-8 US-09-248-796A-14679 US-09-248-796A-10 US-08-915-136-10 US-08-957-310-10 US-10-011-366-10 US-09-248-796A-18993 S1963-04-2 US-07-867-106-3 US-07-867-106-3 US-09-630-822A-62	US-09-005-069-62 US-09-171-156A-21
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866 875 1315 452 366 2366 2366 2366 2366 2366 2366 236	900
31.6 31.6 331.6 229.8 111.7 111.7 111.7 111.7 111.7 111.7 111.7 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 111.1 11	u u
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# AL IGNMENTS

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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                   APPLICANT: Aoki, K. Roger
APPLICANT: Sachs, George
ITILE OF INVENTION: Methods and Compositions for the
ITILE OF INVENTION: Treatment of Pancreatitis
FILE REPERENCE: 17282
CURRENT APPLICATION NUMBER: US/09/288,326A
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 9
IENGTH: 382
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57.6%; Pred. No. 2.4e-42;
tive 26; Mismatches 30
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           Sequence 9, Application US/09288326A Patent No. 6776990 GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 83; Conserv
-09-288-326A-9
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Gaps

Sequence 9, Application US/09548409B
Patent No. 6843998
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Sachs, George
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treament of Pancreatitis
FILLE REFERENCE: 17282CIP(AP)
CURRENT APPLICATION NUMBER: US/09/548,409B US-09-548-409B-9

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APPLICATION NUMBER:
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Sequence 23, Application US/08480604A

Patent No. 5736139

GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER MEDIENE & CARROLL, LLP
STREET: 220 MONTGOWERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STREET: CALIFORNIA
COUNTRY: UNITED STATE:
ZIP.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: U4-APR-1995
RIING DATE: U4-APR-1995
FILING DATE: U4-APR-1995
FILING DATE: U6-APR-1995
FILING DATE: U6-APR-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: U6-APR-1995
PRIOR APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: U6-DEC-1992
FILING DATE: U6-DEC-1992
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57.6%; Pred. No. 2.4e-42;
tive 26; Mismatches 30
                  PRIOR APPLICATION NUMBER: US 09/288,326 BRIOR FILING DATE: 1999-04-08 NUMBER OF SEC ID NOS: 12 SOFTWARE: PASKEN FOR WINDOWS VERSION 3.0
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                                                                                                                                                                            TYPE: PRT ORGANISM: Clostridium botulinum
CURRENT FILING DATE: 2000-04-13
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Best Local Similarity 57.64
Matches 83; Conservative
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                                                                                                                       SEQ ID NO 9
LENGTH: 382
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140 VFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKL 199
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US-08-105-496A-23
Sequence 23, Application US/08405496A
Patent No. 5919665
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NETROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE MEDIENK & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION NUMBER: US/08/405,496A
FILING APPLICATION A24
PRIOR APPLICATION NUMBER: US/08/329,154
FILING BAPLICATION NUMBER: US/08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US/08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US/07/985,321
FILING APPLICATION NUMBER: US/07/985,321
FILING APPLICATION NUMBER: US/07/985,321
FILING APPLICATION NUMBER: US/07/985,321
FILING APPLICATION NUMBER: US/07/985,321
FILING APPLICATION DATA:
APPLICATION NUMBER: US/07/429,791
FILING APPLICATION DATA:
APPLICATION NUMBER: US/07/429,791
FILING APPLICATION DATA:
APPLICATION NUMBER: US/07/429,791
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Best Local Similarity 57.6%; Pred. No. 2.9e-42;
Matches 83; Conservative 26; Mismatches 30
                                              NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE JOSET NUMBER: 0PHD-01763
TELECHONE (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         LENGTH: 438 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: protein US-08-480-604A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VFNYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE CORRESPONDENCES: 32
CORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEM & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 438;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
REGISTRATION NUMBER: 40,027
REPERBNIC/DOCKET NUMBER: OPHD-01308
FELECOMMUNICATION:
TELEPHONE: (415) 397-8338
FILEPAX: (415) 397-8338
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FILEPAX: (415) 397-8
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APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
ON UMBER: US 07/985,321
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Patent No. 6290960
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CALIFORNIA
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140 VFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VENYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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Patent No. 6613329
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE NUMBER OF SEQUENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATR:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                                                                                                                                                                                      57.9%; Score 440.5; DB 2
57.6%; Pred. No. 2.9e-42;
tive 26; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: HAVERSTOCK, MEDLEN & CARROLL.
220 MONTGOMERY STREET, SUITE 2200
                                                                                                           NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | : | : | : | 260 DPNKYVDVNNVGIRGYMYLKGPRG 283
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APPLICATION NUMBER: US 08/329,154
PILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/985,321
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APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                      TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 5/...
Local 83; Conservative
                                                                                                                                                                                                                                                                                              438 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MOLECULE TYPE: protein

US-08-915-136-23
                                                                                                                                                                                                                                                                                                                           amino acid
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US-08-405-496A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 DGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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; Sequence 26, Application US/08480604A
; Patent No. 5736139
; General information;
APPLICANT: KINK, JOHN A.
; APPLICANT: PADHYE, NISHA V.
; APPLICANT: PADHYE, NISHA V.
; APPLICANT: FIRACA, JOSEPH R.
; APPLICANT: FIRACA, JOSEPH R.
; APPLICANT: FIRACES, JOSEPH R.
; APPLICANT: FIRACES, OCCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
; TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSE: MEDIEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.9%; Score 440.5; DB 2; Length 9 Best Local Similarity 57.6%; Pred. No. 2.9e-42; Matches 83; Conservative 26; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01610
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-838
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acide
TYPE: amino acid
TYPE: APPLICATION AND ACID
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PRICE APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
FRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FLING DATE: 16-MAR-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 RIDKSITQNS----NFLNINQQRG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-09-084-517-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-480-604A-26
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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: NEUROTOKIN
TITLE OF INVENTION: NEUROTOKIN
TITLE OF INVENTION: NEUROTOKIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.9%; Score 440.5; DB 1; Best Local Similarity 57.6%; Pred. No. 3.1e-42; Matches 83; Conservative 26; Mismatches 30;
                                               PILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
PELICATION DATA:
PELICATION NUMBER: US 07/985,321
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/429,791
PILING DATE: 31-007-1989
ATTORNEY/AGENT INFORMATION:
RAME: INGOLIA, DIAME E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCRET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 DPNKYVDVNNVGIRGYMYLKGPRG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 RIDKSITONS----NFLNINQORG 139
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
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Patent No. 5919665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-480-604A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 DGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKFYYMLNLY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VENYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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Sequence 26, Application US/09084517

Patent No. 6613329

Patent No. 6613329

APPLICANT: KINK, JOHN A.

APPLICANT: WILLIAMS, JAMES A.

ITILE OF INVENTION: PROCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PROFICE DISEASE

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAVESTYCK, MEDLEN & CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;; Score 440.5; DB.;; Pred. No. 3.1e-42.26; Mismatches 30
                                                           PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTONNEY, AGENT INFORWATION:
NAME: INGOLIA, DIANE E.
REGISTAATION NUMBER: 40,027
REPERECAMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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1. UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/084,517
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APPLICATION NUMBER: US 00
FILING DATE: 16-MAR-1995
                                            25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.6%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MOLECULE TYPE: protein
US-08-915-136-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UN
ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 DGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VPNYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDIEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.9%; Score 440.5; DB 1; Length Best Local Similarity 57.6%; Pred. No. 3.1e-42; Matches 83; Conservative 26; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 0PHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHRACATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 RIDKSITONS----NFLNINOORG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 DPNKYVDVNNVGIRGYMYLKGPRG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
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FILING DATE: 16-MAR-1995
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COMPUTER READABLE FORM:
COMPUTER: Ploppy disk
CMDUTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/08915136
Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                                                    : 462 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-405-496A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAN FRANCISCO
CALIFORNIA
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-915-136-26
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 DGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VFNYTQMISISDYINKWIFVTITNNRLGNGRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
MEDLUM TYPE: PLOPPY disk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Sp. 9%; Score 440.5; DB 2; Length A
Best Local Similarity 57.6%; Pred. No. 3.1e-42;
Matches 83; Conservative 26; Mismatches 30; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION UNBER: US/08/480,604A
FILING DATE: 07-UNN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                         NAME: CARROLL, PETER G.
REGISTRATION UNDER: 32,837
REFERENCE/DOCKET NUMBER: 0PHD-01610
TELECOMMUNICATION INFORMATION:
TELEPHAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-007-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/9429,791
FILING DATE: 31-007-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : | : | : | : | 284 DPNKYVDVNNVGIRGYMYLKGPRG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/08480604A; Patent No. 5736139; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-480-604A-28
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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.9%; Score 440.5; DB 1; Length 1296; Best Local Similarity 57.6%; Pred. No. 1.3e-41; Matches 83; Conservative 26; Mismatches 30; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 28, Application US/08405496A; Patent No. 5919665; GENERAL INFORMATION: WILLIAMS, JAMES A. TITLE OF INVENTION: WACCINE FOR CLOSTRIDIUM BOTULINUM; TITLE OF INVENTION: NEUROTOXIN CORRESPONDENCE ADDRESS: 30 CORRESPONDENCE ADDRESS: ADDRESSEE: MEDLEN & CARROLL, LLP; STREET: 220 MONTCOMERY STREET, SUITE 2200 STREET: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
                                        PEDLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1987
APPLICATION NUMBER: US 07/829,791
FILING DATE: 31-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPHD-01763
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                                                                                                                                                                                                                                                                                                                                                                                                           NAME: INCOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFRENCE/DOCKET NUMBER: OPHD-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-838
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-480-604A-28
                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.9%; Score 440.5; DB 2; Length 1296; 57.6%; Pred. No. 1.3e-41;
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Patent No. 6613329
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE NUMBER OF SEQUENCES:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Mismatches
                                                                                                                                                                                                          PRILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
RILING DATE: 04-DEC-1992
FILING DATE: 04-DEC-1992
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : : | : | : | 1118 DPNKYVDVNNVGIRGYMYLKGPRG 1141
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                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
                                                                                                                                                                                          US 08/329,154
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 705-8410
                                                                                                                                           FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: HAVERSTOCK,
STREET: 220 MONTGOMERY
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.6'
Matches 83; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-915-136-28
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                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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US-09-084-517-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VENYTOMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADINES, NISHA V.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.9%; Score 440.5; DB 1; Length Best Local Similarity 57.6%; Pred. No. 1.3e-41; Matches 83; Conservative 26; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMENY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                CLASSIPICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 424
FILING DATE: 25-0CT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
PRIOR APPLICATION NUMBER: US 08/161,907
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/985,321
PRIOR APPLICATION NUMBER: US 07/995,321
PRIOR APPLICATION NUMBER: US 07/995,321
PRIOR APPLICATION NUMBER: US 07/429,791
PILING DATE: 31-0CT-1989
PILING DATE: 31-0CT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1118 DPNKYVDVNNVGIRGYMYLKGPRG 1141
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APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/08915136
Patent No. 6290960
                                                                                                                                                                                                                                                                                                                                   NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: OF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 397-8338
INFORMATION POR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Gaps 5;

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610 DGCRDPRRYIMIKYFNLFDKELNBKEIKDLYDSQSNSGILKDFWGNYLQYDKPYYMLNLF 669
                                                                                                                                                                                                                                            61 VGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                           1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
                                                                          Query Match 55.7%; Score 423.5; DB 2; Length 848; Best Local Similarity 56.9%; Pred. No. 6.6e-40; Matches 82; Conservative 23; Mismatches 34; Indels 5
                                                                                                                                                                                                                                                                                                                         120 RIDKSITQNSNFLNINQQRGVYQK 143
                                                                                                                                                                                                                                                                                                                                                        2, 2006, 00:49:34
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Job time : 18.7077 secs
                                US-10-360-101-219
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Parent No. 6861236

GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
TILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR PELICATION NUMBER: EP 02077060.8
PRIOR PLICATION NUMBER: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: ParentIn Version 3.1
SEQ ID NO 219
LENGTH: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
RGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sequence A-heavy chain of clostridium botulinum toxin type A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.9%; Score 440.5; DB 2; Length : 57.6%; Pred. No. 1.38-41; tive 26; Mismatches 30; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                            FILLING DALE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/429,791
FILING DATE: 03-OCT-1989
ATTORNEY, AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (4115) 39-838
INFORMATION POR SEQ ID NO: 28:
LENGTH: 1296 amino acids
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US-09-084-517-28
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Best Local Similarity
Matches 83; Conserva
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March 2, 2006, 01:11:03; Search time 57.2993 Seconds (without alignments) 1050.055 Million cell updates/sec
                                                                                                                                                                                                                                   761
1 VFNYTQMISISDYINKWIFV.....ITQNSNFLNINQQRGVYQKP 144
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                               1867569 seqs, 417829326 residues
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                           US-08-981-087B-3
                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                             Run on:
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Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published Applications AA Main: \* /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep: \* ; /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep: \* ; /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep: \* ; /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep: \* ; /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep: \* ; /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep: \* ; /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep: \* ; /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Length	BB	ID	Description
	761	100.0	144	7	US-08-981-087A-3	Sequence 3, Appli
7	761	100.0	431	~	US-08-981-087A-1	Sequence 1, Appli
e	761	100.0	432	m	US-09-910-186A-16	.16
4	761	100.0	432	m	US-09-910-186A-34	
ហ	761	100.0	432	4	US-10-452-024-178	178,
9	761	100.0	645	4	US-10-130-973A-8	
7	191	100.0	645	4	US-10-478-516-5	ญั
80	761	100.0	657	4	US-10-478-516-6	é,
6	761	100.0	657	4	US-10-478-516-7	۲,
10	761	100.0	685	4	US-10-130-973A-7	7.
11	761	100.0	862	4	US-10-130-973A-4	4
12	191	100.0	887	4	US-10-130-973A-6	ģ
13	761	100.0	979	4	US-10-478-516-26	Sequence 26, Appl
14	761	100.0	1032	4	US-10-130-973A-15	12
15	191	100.0	1092	4	US-10-130-973A-14	14
16	761	100.0	1192	4	US-10-478-516-23	Sequence 23, Appl
17	761	100.0	1192	4	US-10-478-516-24	24,
18	761	100.0	1278	4	US-10-452-024-152	Sequence 152, App
19	761	100.0	1278	4	US-10-205-516-12	Seguence 12, Appl
20	761	100.0	1288	4	US-10-205-516-26	
21	632	83.0	1280	4	US-10-452-024-162	162,
22	622	81.7	1268	4	US-10-452-024-156	156,
23	612	80.4	448	4	US-10-354-774-73	73, 7
24	612	80.4	448	4	US-10-271-012-73	73,
25	612	80.4	448	4	US-10-729-122-73	Sequence 73, Appl
56	612	80.4	448	4	US-10-729-039-73	Sequence 73, Appl
27	612	80.4	448	Ŋ	US-10-729-527-73	73,

Appl Appl Appl Appl Appl Appl Appl Appl		
73, 73, 71, 71, 71, 71, 71, 71, 71, 71, 71, 71		
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10-727-898 10-728-696 10-354-744 10-371-012 10-472-024 10-729-039 10-729-696 10-728-696 10-728-696 10-728-696 10-728-696 10-728-696 10-729-012 10-729-012 10-729-012 10-729-012	C. C. Alth 1409	89
	uS/08981087A 081304A1 Michael J we, Margaret L. Nigel P. K, Vladimir A. TYPE F BOTULINUM SSS: E VANDERHYE P.C. US20020081304A1th NPY disk compatible compa	7 24-68i
	9 m m m m m m m m m m m m m m m m m m m	3: 32 33: 33: 33: 33: 33: 33: 33: 33: 33
00004444444400000000000000000000000000	US/08981087A 81304A1 iichael J. iigel P. iigel P. iigel P. r. Vladimir A r. Vladimir A r. Vladimir A r. Vladimir A r. Vladimir A r. Vladimir A r. VanderHyE P iS20020081304 is vanderHyE P rocompatible pompatible pompatible pompatible pompatible recooksins-DC r. Release #1. uS/08/981, r. VI998 r. PCT/GB96/C	MA-199 AATION TCHUI REER 28 MMBER 26 MO: 1100 NO: CICS: acide
44448 1122748 122748 1227448 12274444 122744444 152224444444444	plication US/0898108 US20020081304A1 MATION: Elmore, Michael J. Bauchline, Margaret Minton, Nigel P. Passchnik, Vladiam, Titball, Richard W. Titball, Richard W. VENTION: TYPE F BOT EQUENCES: EQUENCES: INCE ADDRESS: INCE ADDRESS: INCE ADDRESS: INCE ADDRESS: INCE ADDRESS: Ingron ON TOWN E VANDERHYE Ingron ON TOWNEY FE: 12-744 FE: Floppy disk USAA ON TOWNEY: PC-DOS/MS- Patentin Release # LICATION: 424 CATION: 424	DATE: 12-JUN-1995 AGENT INFORMATION: CLEAWEDGA, AITHUR R. ATION NUMBER: 25,327 ICE/DOCKET NUMBER: 12 MICATION INFORMATION: NE: 703-816-4000 I: 703-816-4100 I: FOR SEQ ID NO: 3: CHARACTERISTICS: 144 amino acids amino acid amino acid sumino acids into acid sumino acids into acid into aci
***	plication . US2002/ . US2002/ . US2002/ . US2002/ . Manton, . Paschn: . Titbachn: . Titbachn: . Ill00 No Ill00 No Illngton . USA . U	: 12-JJ TI INFORM TI ON NUMBER OCKET NN TION INI O3-816-1. SEQ ID ACTERIS' SEQ ID ACTERIS' SEQ ID SE
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612 612 612 612 612 612 612 612 7.5 7.5	T 1  101-087A-3  1020c1 3, Application US/0894  11cation No. US20020081304A.  MERAL INFORMATION:  APPLICANT: Blmore, Michael APPLICANT: Minton, Nigel P  APPLICANT: Minton, Nigel P  APPLICANT: Pasechnik, Vlad.  APPLICANT: Pasechnik, Vlad.  APPLICANT: Alball, Richart  TITLE OF INVENTION: TYPE F  CONTESPONDENCES: 6  CORRESPONDENCES: 6  COUNTRY: USA  ZIP: 22201-4741  COMPUTER: VA  ZIP: 22201-4741  COMPUTER: LAPPLICATION DATA:  MEDIUM TYPE: Floppy disk  COMPUTER: BADLABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: BADLABLE FORM:  MEDIUM TYPE: Patentin Relea  CURSTRICATION UNMERR: US/OF  FILING DATE: 27-WAY-1998  CLASSIFICATION NUMBER: PCT/A  PRILOR APPLICATION DATA:  APPLICATION NUMBER: PCT/A  RILING DATE: 12-UNN-1996  FILING DATE: 12-UNN-1996  FILING DATE: 12-UNN-1996  PRILOR APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICANTON DATA:  APPLICANT	FILING DATE: 12-JUN-199; ATTORNEY, AGENT INFORMATION NAME: Crawford, Arthur 12, REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER: 25, TELECOMMINICATION INFORMATI TELECHONE: 703-816-4100 FORMATION FOR SEQ ID NO: 500 TO TELEFAX. 703-816-4100 FORMATION FOR SEQ ID NO: 500 TO TELEFAX. 703-816-4100 FORMATION FOR SEQ ID NO: 500 TELEFAX. 703-816-4100 FORMATION FOR SEQ ID NO: 500 TELEFAX. 703-816-4100 STRANDEDNESS: 100 acid STRANDEDNESS: 100
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1  US-08-981-087A-3  US-08-901-081A-3  SEQUENCE 3, Application US/089, Publication No. US20020081304A  GENERAL INFORMATION:  APPLICANT: Bimore, Michael APPLICANT: Minton, Nigel PAPLICANT: Minton, Nigel PAPLICANT: Titball, Richart TILE OF INVENTION: TYPE F NUMBER OF SEQUENCES: 6  CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON & VANDE STREET: 1100 No. US20020 CITY: Arlington STREET: VA  ZIP: 22201-441  COMPUTER: VA  ZIP: 22201-441  COMPUTER: IRM PC compation PRICATION NUMBER: US/OFTWARE: Patentin Releast CURSTRICATION NUMBER: US/OFTWARE: PAPLICATION NUMBER: PCT/APPLICATION NUMBER: PCT/APPLICATION NUMBER: PCT/APPLICATION NUMBER: PCT/APPLICATION NUMBER: PCT/APPLICATION NUMBER: PCT/APPLICATION DATA: APPLICATION NUMBER: PCT/APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLING APPLICATION DATA: REPLI	ATTORNEY PATTORNEY PATTORNEY PATTORNEY PEGISTRA REFERENCY TELECOMMUNT TELECOMMUNT TELEPAX: INFORMATION SEQUENCE C LENGTH: STYRE STYRE STYRE TOPOLOGY MOLECULE TOPOLOGY
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                                                                                                                   1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
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      Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Elmore, Michael J.
APPLICANT: Mauchline, Margaret I.
APPLICANT: Manchine, Margaret I.
APPLICANT: Minton, Nigel P.
APPLICANT: Paschnik, Vladimir A.
APPLICANT: Titball, Richard W.
TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US200200081304Alth Glebe Rd. 8th floor
                                               0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,087A
FILING DATE: 12-MAY-1998
CLASSIFICATION TYPER: 12-MAY-1998
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 28 9511909.5
FILING DATE: 12-JUN-1995
ATTONNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 25,327
REBERENCE/DOCKET NUMBER: 124-688
TELECOMMUNICATION INFORMATION:
TELEFRAK: 703-816-4100
TANDEMATICATION INFORMATION:
TELEFRAK: 703-816-4100
TANDEMATICATION INFORMATION:
TELEFRAK: 703-816-4100
  100.0%; Score 761; DB 2;
100.0%; Pred. No. 8.5e-71;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          TDKSITQNSNFLNINQORGVYQKP 144
                                                                                                                                                                                                                                                                   121 TDKSITQNSNFLNINQQRGVYQKP 144
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Query Match
Best Local Similarity 100.
Matches 144; Conservative
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STATE: VA
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145 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 204
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100.0%; Score 761; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 144; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROTOSIN
TITLE OF INVENTION: NEUROTOSIN
FILE REFERENCE: A33626-A
GOTOSIN
CURRENT PILING DATE: 2001-07-20
CURRENT FILING DATE: 2001-07-20
PRIOR PELICATION NUMBER: OF/11,419
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 09/611,419
PRIOR APPLICATION NUMBER: 09/611,419
PRIOR PILING DATE: 1999-05-12
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PRIOR APPLICATION NUMBER: 60/133,869
PRIOR PILING DATE: 1999-05-12
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; Sequence 34, Application US/09910186A
; Sequence 100 No. US20030009025A1
; GENERAL INPORMATION:
; APPLICANT: U.S. Army Medical Research & Material Command
                                                                                                                                                                                                                                                            121 TDKSITQNSNFLNINQQRGVYQKP 144
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US-09-910-186A-16
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APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
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Publication. No. US20040208889A1
GENERAL INFORMATION:
APPLICANT: Sutron, John M.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REPERBINE: 1581:1000000
CURRENT APPLICATION NUMBER: US/10/478,516
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Best Local Similarity 100.0%; Pred. No. 3.4e-70; Matches 144; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/GB00/04644
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR PILING DATE: 2000-04-07
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SOFTWARE: Patentin version 3.0
SEQ ID NO B
LENGTH: 645
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Best Local Simi
Matches 144;
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US-10-478-516-5
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APPLICANT: Maksymowych, Andrew
TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport
FILE REFERENCE: 9855-96Ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VGCNDTRYVGIRYFKVFDTBLGKTBIFTLYSDBPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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  IIILE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM IIILE OF INVENTION: NEUROFOXIN
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100.0%; Score 761; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.4e-70;
Matches 144; Conservative 0; Mismatches 0;
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                                             THIER REFERENCE: A33626-A 067252.0107
CURRENT APPLICATION NUMBER: US/09/910,186A
CURRENT PILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/0800/12890
PRIOR FILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-07-06
PRIOR FILING DATE: 1999-05-12
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PRIOR FILING DATE: 1993-09-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
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Sequence 178, Application US/10452024

Publication No. US20040013687A1

GENERAL INFORMATION:
APPLICANT: Simpson, Lance
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PRIOR APPLICATION NUMBER: 60/133,873
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 178
LENGTH: 432
TYPE: PRT
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sequence 7, Application US/10130973A

sequence 7, Application US/10130973A

publication No. US20030147895A1

GENERAL INFORMATION:
APPLICANT: Shone, Clifford
APPLICANT: Staten, John
APPLICANT: Staten, John
APPLICANT: Staten, Soliford
APPLICANT: Staten, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.092080.
CURRENT APPLICATION NUMBER: US/10/130,973A

CURRENT FILING DATE: 2002-10-21

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn version 3.0

SEQ ID NO 7

LENGTH: 685
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          Sequence 7, Application US/10478516

Sequence 7, Application US/10478516

Publication No. US2004020889A1

GENERAL INFORMATION:

APPLICANT: Sutton, John M.

APPLICANT: Shone, Clifford C.

TITLE OF INVENTION: Paramaceutical Use of Secreted Bacterial Effector Proteins

FILE REFERENCE: 1581.1000000

CURRENT APPLICATION NUMBER: US/10/478,516

PRIOR PILING DATE: 2003-11-24

PRIOR APPLICATION NUMBER: GB 0112687.9

PRIOR APPLICATION NUMBER: GB 0112687.9

PRIOR PILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Version 3.1
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100.0%; Score 761; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.1e-70;
Matches 144; Conservative 0; Mismatches 0;
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100.0%; Score 761; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 144; Conservative 0; Mismatches 0;
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US-10-478-516-6
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APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
TITLE OF INVENTION: PLANDER: US/10/478,516
CURRENT APPLICATION NUMBER: US/10/478,516
PRIOR APPLICATION NUMBER: PC/GB02/02384
PRIOR PILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 657
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100.0%; Score 761; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 144; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                               Length 645;
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Best Local Similarity 100.0%; Pred. No. 5.6e-70;
Matches 144; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2002-05-21
PRIOR PEPLICATION NUMBER: GB 0112687.9
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SPFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 645
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ORGANISM: Artificial sequence
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OTHER INFORMATION: Protein sequence for YopT, factor Xa linker, diphtheria toxin, OTHER INFORMATION: translocation, OTHER INFORMATION: domain, with BONT/F-HC US-10-478-516-26
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APPLICANT: Station, John M.
APPLICANT: Station, John M.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
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100.0%; Pred. No. 9.5e-70;
ive 0; Mismatches 0; Indels
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Pred. No. 8.4e-70;
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Publication No. US20040208889A1
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 0080;
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
; SRQ ID NO 6
; LENGTH: 887
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Best Local Similarity 100.0%;
Matches 144; Conservative 0
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ORGANISM: Artificial Sequence
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Matches 144; Conservative
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LENGTH: 979
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APPLICANT: Shone, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERENCE: 1581.0920000
CURRENT PILING DATE: 2002-10-21
FRIOR PILING DATE: 2002-10-21
FRIOR PELICATION NUMBER: CB 9928530.6
FRIOR FILING DATE: 1999-12-02
FRIOR FLING DATE: 1999-12-02
FRIOR FLING DATE: 2000-04-07
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Publication No. US20030147895A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shone, Clifferd
APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPERBNCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: ET/GB00/04644
PRIOR APPLICATION NUMBER: GB 9928530.6
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Best Local Similarity
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                                                                         Sequence 15, Application US/10130973A

PUDICATION NO. US20030147895A1

GENERAL INFORMATION.

APPLICANT: Shone, Clifford

APPLICANT: Silan, Niden

APPLICANT: Silan, Niden

TITLE OF INVENTURI Constructs for Delivery of Therapeutic Agents to Neuronal Cells

FILE REFERENCE: 1581.0920000

CURRENT APPLICATION NUMBER: US/10/130,973A

CURRENT PILING DATE: 2002-10-21

PRIOR FILING DATE: 2002-12-04

PRIOR PILING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0

SEQ ID NO 15

LENGTH: 1032

TYPE: PRI

VERSION NOS: 18

CREATION NOS: 18

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| Sequence 14, Application US/10130973A
| Sequence 14, Application US/10130973A
| Publication No. US20030147895A1
| Publication No. US20030147895A1
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| APPLICANT: Sutton, John
| TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
| TITLE OF INVENTION: Constructs (US/10/130, 973A
| TITLE OF INVENTION NUMBER: DS/10/130, 973A
| CURRENT FILING DATE: 2002-10-21
| PRIOR FILING DATE: 2000-12-04
| PRIOR FILING DATE: 1999-12-02
| PRIOR PILING DATE: 2000-04-07
| PRIOR FILING DATE: 2000-04-07
| PRIOR FILING DATE: 2000-04-07
| PRIOR FILING DATE: 2000-04-07
| PRIOR FILING DATE: 2000-04-07
| PRIOR FILING DATE: 2000-04-07
| PRIOR FILING DATE: DOWN OF SOME SOME SOFTWARE: Patentin version 3.0
| SEQ ID NO 14
| LENTTH: 1092
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Best Local Similarity 100.0%; Pred. No. 1e-69;
Matches 144; Conservative 0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TDKSITQNSNFLNINQQRGVYQKP 144
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RESULT 14
US-10-130-973A-15
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Gaps

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 144; Conservative 0; Mismatches 0; Indels 0;

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| Db | 806 | VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 865 |
| QY | 61 | VGCNDTRYVGIRYFKVPDTELGKTEIFTLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120 |
| Db | 866 | VGCNDTRYVGIRYFKVPDTELGKTEIFTLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 925 |
| QY | 121 | TDKSITQNSNFLNINQRGYYQKP 144 |
| Db | 926 | TDKSITQNSNFLNINQRGYYQKP 949 |
| Search completed: March 2, 2006, 01:17:48 |
| Job time : 58.2993 secs
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1 VFNYTQMISISDYINKWIFVTITNWRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60

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March 2, 2006, 01:12:18; Search time 5.84687 Seconds (without alignments) 491.279 Million cell updates/sec
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761
1 VFNYTQMISISDYINKWIFV.....ITQNSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA_New:*

1: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133702 segs, 19947517 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		d			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	88	ID	Description
-	761	100.0	1059	-	US/11/062	Sequence 5, Appli
10	761	100.0	1084	7	US/11/062	8, 2
וה	612	80.4	838	9	US-10-909-769-28	Sequence 28, Appl
4	497.5	65.4	829	ø	US-10-909-769-26	Sequence 26, Appl
5	440.5	57.9	849	9	US-10-909-769-18	18,
•	440.5	57.9	1067	7	US/11/062	Sequence 3, Appli
7	440.5	57.9	1092	7	US/11/062	Sequence 6, Appli
80	296.5	39.0	855	9	US-10-909-769-30	Sequence 30, Appl
6	296	38.9	900	9	US-10-909-769-20	20,
10	284.5	37.4	1070	7	US/11/062	4,
11	284.5	37.4	1095	7	US/11/062	Sequence 7, Appli
12	284.5	37.4	1169	7	US-11-077-550-20	20
13	245.5	32.3	834	ø	US-10-909-769-24	24, 7
14	240.5	31.6	1315	7	US-11-077-550-141	Sequence 141, App
15	239	31.4	842	9	US-10-909-769-22	Sequence 22, Appl
16	89	11.7	2367	7	US-11-051-453-42	42, Ag
17	76.5	10.1	1356	7	US-11-129-741-2939	Sequence 2939, Ap
18	76.5	10.1	1356	7	US-11-129-741-2941	Sequence 2941, Ap
19	76.5	10.1	1356	7	US-11-129-741-2943	Sequence 2943, Ap
20	76.5	10.1	1356	~	US-11-129-741-2945	Sequence 2945, Ap
21	76.5	10.1	1356	7	US-11-129-741-2949	Sequence 2949, Ap
22	76.5	10.1	1356	7	US-11-129-741-2951	Sequence 2951, Ap
23	76.5	10.1	1356	7	US-11-129-741-4245	4245,
24	76.5	10.1	1362	9	t	420,
25	76.5	10.1	1362	7	US-11-129-741-420	Sequence 420, App

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2937, Ap 3655, Ap 10796, A 2, Appli	7, Appli 2947, Ap 8, Appli 10150, A	230, App 230, App 240, App 4284, Ap	351, App 200, App 2330, Ap	3028, Ap 8258, Ap 10448, A 5, Appli
Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence
US-11-129-741-2937 US-11-129-741-3655 US-11-098-686-10796 US-10-926-709-2	US-10-926-709-7 US-11-129-741-2947 US-10-926-709-8 US-11-098-686-10150	US-11-087-099-2275 US-11-052-554A-230 US-11-052-554A-240 US-11-087-099-4284 US-11-087-099-4284	US-10-485-517-218 US-10-485-517-351 US-11-485-517-200 US-11-087-099-2330	US-11-087-099-3028 US-11-087-099-8258 US-11-087-099-10448 US-10-959-322-5
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26 27 28 29	30 33 33	3 3 3 4 4 7 5 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	8 6 4 4 8 6 0 1	4 4 4 4 2 6 4 8

# ALIGNMENTS

a linker,

RESULT 2 US/11/062

12

2

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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei-Jon
APPLICANT: Aoki, Kei-Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterism
FILE REFERENCE: ALLEGOID-100 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18
LENGTH: 849
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Acis, Kei-Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLEO10-10.0 (ROI2003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SSC THARE: PatentIn version 3.3
SEQ ID NO 26
LENGTH: 829
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     61 VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.4%; Score 497.5; DB 6; Best Local Similarity 68.1%; Pred. No. 1.7e-41; Matches 94; Conservative 21; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Amino acid sequence of HC US-10-909-769-26
                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                      121 TDKSITQNSNFLNINQQRGV 140
                                                                                                                                                                                                                    678 KDKYITLNSGILNINQQRGV 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 18, Application US/10909769; Publication No. US20060024331A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 DKSI-TQNSNFLNINQQR 138
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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US-10-909-769-18
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Publication No. US20060024331A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLEOO10-100 (ROIZO03-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 28
LENGTH: 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human US/11/062,471A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                           APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
APPLICANT: HALLIS, Baseam
APPLICANT: HALLIS, Baseam
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 1990-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1998-11-05
PRIOR PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SOPTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 761; DB 7; Length 1084; 100.0%; Pred. No. 2e-67; cive 0; Mismatches 0; Indels 0
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82.9%; Pred. No. 8e-53;
tive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDKSITONSNFLNINQQRGVYQKP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDKSITQNSNFLNINQQRGVYQKP 941
Sequence 8, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
                                                                             APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.9*
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1084
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1 VPNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60

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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human Mi
US/11/062,471A-6
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Uen
APPLICANT: Lin, Wei-Uen
APPLICANT: Acki, Kei Roger
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLEGOID-100 (RO12003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30
LENGTH: 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLANLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILER REFERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/31,050
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1092;
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39.0%; Score 296.5; DB 6;
Best Local Similarity 49.6%; Pred. No. 1.3e-21;
Matches 58; Conservative 22; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

57.9%; Score 440.5; DB 7;

Best Local Similarity 57.6%; Pred. No. 1e-35;

Matches 83; Conservative 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 RTDKSITQNS----NFLNINQQRG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | : | : | |
914 DPNKYVDVNNVGIRGYMYLKGPRG 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-909-769-30
; Sequence 30, Application US/10909769
; Publication No. US20060024331A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
John Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker, US/11/062,471A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VGCNDT-RYVGIRYFKVPDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
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                                                                                                                                                                                                                                             APPLICANT: SHONE. Clifford Charles
APPLICANT: STONE. Clifford Charles
APPLICANT: STONE. Clifford Charles
APPLICANT: STIMAN: Nigel
APPLICANT: ALLIS, Bassam
APPLICANT: STIMAN: Nigel
TITLE OF INVERTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVERTION: Delivery of Superoxide Dismutase to Neuronal Cells
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: OF/GB99/03699
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR FILING DATE: 1998-11-05
SRIOR FILING DATE: 1998-11-05
SRIOR FILING DATE: 1998-11-05
SRIOR FILING DATE: 1998-11-05
SRIOR FILING DATE: 1998-11-05
SROFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                        61 VGCNDT-RYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                       1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
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                                                                                                           Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

57.9%; Score 440.5; DB 7; Length

Best Local Similarity 57.6%; Pred. No. 9.7e-36;

Matches 83; Conservative 26; Mismatches 30; Indels
                                                                                                         57.9%; Score 440.5; DB 6; Length llarity 57.6%; Pred. No. 7.4e-36; Conservative 26; Mismatches 30; Indels
                                 CTHER INFORMATION: Amino acid sequence of HC US-10-909-769-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 RIDKSITONS----NFLNINQORG 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                 120 RIDKSITONS----NFLNINOORG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/11062471A Publication No. US20050255093A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                      Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1067
             FEATURE:
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US/11/062
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, OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human 0S/11/062,471R-7
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APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Migel
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal
CURRENT FILING DATE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT APPLICATION NUMBER: 09/831,050
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NOS: 11
SEQ ID NOS: 12
FEMALE. PATENTIAL OF SECOLET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SECONET OF SE
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                                                                                                                   Indels
                                                           DB 7;
                                              Query Match
37.4%; Score 284.5; DB 7
Best Local Similarity 39.3%; Pred. No. 2.6e-20;
Matches 59; Conservative 27; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                           119 -----IRTDKSI-----TQNSNFLN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                    885 KNSYIKLKKDSPVGEILTRSKYNQNSKYIN 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              910 KNSYIKLKKDSPVGEILTRSKYNONSKYIN 939
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; APPLICANT: Shone, Clifford Charles; APPLICANT: Quinn, Conrad Padraig; APPLICANT: Poster, Keith Alan; APPLICANT: Chaddock, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/11062471A
Publication No. US20050255093A1
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Best Local Similarity 39.3%
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-077-550-20
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                                                                                                                                                                                                                                                      APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei Jen
APPLICANT: Lin, Wei Jen
APPLICANT: Lin, Wei Jen
APPLICANT: Acki Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REPERENCE: ALLEOUO (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTMARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 900
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THER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker,
US/11/062,471A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          655 GDVDRTQFIWMKYFSIFNTQLNGSNIKEIYKIGSYSEYLKDFWGNPLMYNKEYYMFNAGN 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.9%; Score 296; DB 6; Length 900
39.9%; Pred. No. 1.6e-21;
Live 29; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             715 KNSYIKLVKDSSVGEILIRSKYNQNSNYIN---YRNLY 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 -----LRIDKSI------TONSNFLNINQQRGVY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Amino acid sequence of HC
                                                                                                                                                                           Sequence 20, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT CRGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 39.94
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-909-769-20
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604 DENIDENQMLWIRDENIFSKELSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDN 663
                                                                                                                                                           61 -VGCNDTRYVGIRYFKVFDTELGKTEIETLYSDBPDPSILKDFWGNYLLYNKRYYLLNLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 NKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGC-NDTRYVGIRY
                                                     1 VFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130004
CURRENT APPLICATION UNMER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/GB97/02273
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/782,893
PRIOR PILING DATE: 1996-12-27
PRIOR PLING DATE: 1996-12-27
PRIOR PLING DATE: 1996-12-13
PRIOR PLING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR PILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 1/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PLICATION NUMBER: 10/241,596
PRIOR PLILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: 09/255,829
PRIOR FILING DATE: 1999-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 141, Application US/11077550 Publication No. US20050244435A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quinn, Conrad Padraig
Foster, Keith Alan
Chaddock, John
Marks, Phillip
Sutton, J. Mark
Stancombe, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shone, Clifford Charles
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                                                                                                                                                                                                                                                                                                                       120 RTDKSITONSNFLNINO 136
                                                                                                                                                                                                                                                                                                                                                                                                    664 YIDRYİAPESNVLVLVQ 680
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SEQ ID NO 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 42.0%
Matches 47; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei-Jen
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALLEO110-100 (RO12003-146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCND-TRYVGIRYFKVPDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNL-- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.4%; Score 284.5; DB 7; Best Local Similarity 39.3%; Pred. No. 2.9e-20; Matches 59; Conservative 27; Mismatches 45;
                                                                                                              APPLICANT: STANCOMOB, PATILICK
APPLICANT: STANCOMOB, PATILICK
APPLICANT: STANCOMOB, PATILICK
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REPERENCE: 1581.0130004
CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: O9/255,829
PRIOR APPLICATION NUMBER: 08/785,839
PRIOR APPLICATION NUMBER: 1996-02-23
PRIOR APPLICATION NUMBER: 1996-12-27
PRIOR APPLICATION NUMBER: GB652596.5
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR APPLICATION NUMBER: GB9617671.4
PRIOR PLING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 179
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; OTHER INFORMATION: Amino acid seqence of HC US-10-909-769-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
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Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Clostridium botulinum US-11-077-550-20
                                                     Sutton, J. Mark
Stancombe, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.3
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LENGTH: 834
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LENGTH: 11
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TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist FILE REFERENCE: ALLEO10-100 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
TYPE: PRI
ORANISM: Artificial sequence
CRANISM: Artificial sequence
CRANISM: Artificial sequence of HC
US-10-909-769-22
                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                                                                                                                                                                   Query Match
31.4%; Score 239; DB 6; Length 842;
Best Local Similarity 37.0%; Pred. No. 6.3e-16;
Matches 54; Conservative 25; Mismatches 57; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 YYLLNLLRTDKSITQNSNFLNINQOR 138
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Search completed: March 2, 2006, 01:18:30 Job time : 6.84687 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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protein search, using sw model OM protein // Search time 68.5139 Seconds
(without alignments)
917.057 Million cell updates/sec 2, 2006, 00:31:42 March Run on:

US-08-981-087B-4 757 Title:

1 NIFSNTRLYTGVEVIIRKNG......TSSNGCFWSFISKEHGWQEN 143 Perfect score: Sequence:

Scoring table:

2443163 seqs, 439378781 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

geneseqp2003as:\* geneseqp2003bs:\* A Geneseq 21:\* .: geneseqp1990s:\* : geneseqp1990s:\* geneseqp2004s:\* geneseqp2005s:\* geneseqp2001s:\*geneseqp2002s:\* geneseqp2000s: .. .. **Database** :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

COLUMNIC	DB ID Description	2 AAW09017 Aaw09017 Immunogen	2 AAW09014 Aaw09014	4 AAB04103 Botulism	4 AAB04096 Aab04096	4 AAE07894 Aae07894	6 AAE35692 Aae35692 DipT HN	6 AAE35693 Aae35693	6 AAE35694 Aae35694	4 AAE07893 Aae07893	4 AAE07890 Aae07890 Modified	7 4 AAE07892 Modified	6 AAE35713 Aae35713 BONT/F-HC	4 AAE07901	3 AAY93309	3 AAY93312 A m	4 AAE07900 Aae07900	6 AAE35711 BONT/F-HC	6 AAE35710	3 AAY77138 Synthetic	2 AAW68399	9 4 AAB04095 Aab04095 Botulism	3 AAY77137 Aay77137	
	Query Match Length DB	100.0 143	_	100.0 432	100.0 432	100.0 645	100.0 645	100.0 657	100.0 657	100.0 685	100.0 862		100.0 979	100.0 1032		100.0 1084	100.0 1092	100.0 1192	100.0 1192	98.2 432	80.2 448	53.0 419	53.0 449	0 0
*	On Score Ma	757 10	757 10										757 10			757 10		•			607 B	401 5	401 5	
	Result No.		8	m	4	w	9	7	80	6	10	11	12	13	14	15	16	17	18	.19	20	21	22	ć

451 2 AAW68395 74 9 ADZ36069 73 9 ADZ36073 206 3 AAY77144 382 3 AAR77144 415 4 AAB04089 435 4 AAB04089 437 4 AAB04088 438 2 AAR86391 4462 2 AAR86390 462 2 AAR86390 462 2 AAR86390 462 2 AAR86390 462 2 AAR86390 462 2 AAR86390 465 2 AAR863307 4067 3 AAY33307	0	_		Aay77144 Botulinum		Adw24418 C botulin	Adz60271 BONT/A pr				Aab04090 Botulism		Aar95008 Type A ne		Aay77134 Synthetic	Aaw68391 Clostridi	-	Aaw68390 Clostridi	Adz69764 Botulinum	Aay93307 A mangane	Aay93310 A mangane
14E 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AAW68395	ADZ36069	ADZ36073	AAY77144	AAB36303	ADW24418	ADZ60271	AAB04083	ADZ60276	AAB04089	AAB04090	AAB04088	AAR95008	AAW68389	AAY77134	AAW68391	AAR95009	AAW68390	ADZ69764	AAY93307	AAY93310
	11 2	4 9	73	90	32 3	32 9	32 9	5.4	52	14 4	35 4	17 4	438 2	438 2	438 3	15 2	462 2	462 2	859 9	57 3	092 3
	49.5	48.3	46.3	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5
4444444444444444444444 98890000000000000	374.5	366	350.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5
	25	26	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

# ALIGNMENTS

Botulinum toxin; neurotoxin; BoBT/F; immunogen; vaccine; botulism. Immunogenic type F botulinum toxin polypeptide (aa1136-1278). Clostridium botulinum; type F strain Langeland AAW09017 standard; protein; 143 AA 96WO-GB001409. (revised)
(first entry) 17-OCT-2003 31-MAR-1997 WO9641881-A1. 27-DEC-1996. AAW09017; RESULT 1

12-JUN-1996;

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

95GB-00011909.

12-JUN-1995;

Pasechnik VA; Elmore MJ, Mauchline ML, Minton NP, 

WPI; 1997-065467/06.

Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.

Claim 5; Page 19; 37pp; English.

Novel polypeptides (AAM09014-17) respectively comprise amino acids 848-1278, 848-991, 992-1135 and 1136-1278 in the heavy chain of a type F botulinum neurotoxin (BoNT/F). They lack the Lothain and HN epitopes necessary for metalloprotease activity and toxin internalisation. They are free of botulinum toxin activity but can induce protective immunity to a type F botulinum toxin, making them useful for vaccine prodn. Recombinant polypeptides can be produced in transformed host cells, as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 143 AA;

Query Match

100.0%; Score 757; DB 2; Length 143;

408

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Best Local Matches 14

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61 KIIKLIRTSNSNNSLGQIIVWDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                        349 KIIKTIRTSNSNNSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYNNI
                                                                                                                                                                                                                                                                                               Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                   Botulism toxin heavy chain C-terminal sequence (serotype F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Middlebrook JL, Lapenotiere H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                              431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 18b; 73pp; English.
                                                                                                                                                                          Ä
                                                                121 RKNTSSNGCFWSFISKEHGWQEN
                                                                                          409 RKNISSNGCFWSFISKEHGWQEN
                                                                                                                                                                          AAB04103 standard; protein; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0133865P.
99US-0133866P.
99US-0133867P.
99US-0133868P.
99US-0133869P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0146192P
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith LA, Byrne MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-016048/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy chain of bo
against botulism.
                                                                                                                                                                                                                                                                                                                                                                                                              WO200067700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
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12-MAY-1999;
12-MAY-1999;
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                                                                                                                                                                                                                                        11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-2000
                                                                                                                                                                                                                                                                                                                                    infection.
                                                                                                                                                                                                                                                                                                      Botulism;
                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                         AAB04103;
                                                                                                                                             RESULT 3
                                                                                                                                                             AAB04103
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                                                                                                                                   KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLIGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (AAW09014) comprises the heavy chain (amino acids 848-1278)
                                                                                                                 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a type F botulinum neurcoxin (BONT/F), and can be produced using a synthetic gene (AAT48101) based on the natural gene sequence (AAT48100) for the heavy chain. The polypeptides and its fragments (see also AAW9015-17) lack the light chain and HN epitopes necessary for botulinum toxin activity and toxin internalisation. They are free of botulinum toxin, making them useful for vaccine produ. Recombinant polypeptides can be produced in transformed host calls, esp. as fusion proteins, e.g. with maltose binding protein to facilitate purification. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic type F botulinum toxin polypeptide(s) - allows recombinant vaccine prodn.
                                                                     1 NIFSNIRLYTGVEVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                     1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Botulinum toxin; neurotoxin; BOBT/F; immunogen; vaccine; botulism.
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100.0%; Score 757; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 143; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic type F botulinum toxin heavy chain (aa848-1278).
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasechnik VA;
                         ö
         Pred. No. 4.4e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium botulinum; type F strain Langeland
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minton NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                      RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 16-17; 37pp; English.
                                                                                                                                                                                                                                                                                          AAW09014 standard, protein, 431 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB001409
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           100.001
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                         Conservative
                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-065467/06.
N-PSDB; AAT48100.
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9641881-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1996;
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31-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-1996.
                                                                                                                                                                                                                                                                                                                         AAW09014;
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and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an transformed cells to produce peptide antigens useful for eliciting an which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of the combinant nucleic acids are advantageous since it eliminates the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G
New nucleic acids encoding the carboxy- or amino-terminal portions of the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 757; DB 4;
Pred. No. 1.8e-70;
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Best Local Similarity
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RESULT 4 **AAB**04096

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Clostridium botulinum serotypes A-G
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514643/56.
                                Sequence 432 AA;
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01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                              AAE07894;
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                                                                                                                                                                                                                                                                                             410
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ID AAEC
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SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a capacity chain and a 100 kDa light chain which remain linked by a capacity chain of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant corganisms such as Escherichia coli or Pichia pastoris. The use of the recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from
 ö
                                                      350 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNPQNNNGGNIGLGFHSNNLVASSWYYNNI 409
                                                                                                 61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                  1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding the carboxy- or amino-terminal portions of theavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine against botulism.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
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                                                                                                                                                                                                                                                                                                                                                                                 Botulism toxin heavy chain C-terminal sequence (serotype F).
 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND
   0; Mismatches
                                                                                                                                                                                   410 RKNTSSNGCFWSFISKEHGWQEN 432
                                                                                                                                                                  RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                   AAB04096 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 9b; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0133865P.
99US-013386P.
99US-0133867P.
99US-0133868P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US012890.
                                                                                                                                                                                                                                                                                                                                                  (first entry)
     Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-016048/02.
N-PSDB; AAA54490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200067700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-2000;
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29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                   AAB04096;
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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain about into the neuronal cell, where the translocation domain is not a MN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                    ö
                                                                                                                                                                               350 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGELGFHSNNLVASSWYYNNI 409
                                                                                                                                                                                                                                                                     KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.
                                                                                                                                     1 NIFSNITRLYTGVEVLIRKNGSTDISNITDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                           Gaps
                                                                           ö
   Length 432;
                                                                        Indels
                                                                           .
          Score 757; DB 4;
Pred. No. 1.8e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified clostridial heavy chain fragment #1.
                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                          RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 44; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE07894 standard; protein; 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silman N;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2000; 2000WO-GB004644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
Query Match
Best Local Similarity 100.0
Matches 143; Conservative
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and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain fragment. This sequence is constructed by fusing the binding domain of botulinum neurotoxin type F (BONT/F) with translocation domain of diphtheria neurotoxin. (Updated on
                                                                                                                                                                                                                                                                                  61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                           622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells, killing cells, promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection, Prion disease, Alzheimer' disease, hypersecretion disorder; muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospam; asthma; fusion protein; diphtheria toxin; translocation domain; HN domain; DipT; Hc; botulinum type F neurotoxin; binding domain; BONT/F.
                                                                                                                                                                                                                                    1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis; therapy; inflammatory mediator; intracellular trafficking;
                                                                                                                                                                                  ;
0
                                                                                                                                          100.0%; Score 757; DB 4; Length 645; 100.0%; Pred. No. 3e-70; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DipT HN domain-BoNT/F-Hc fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; Page 57-60; 130pp; English.
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                                                                                                                                                                                                                                                                                                                                                         RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                 623 RKNTSSNGCFWSFISKEHGWQEN 645
                                                                      11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE35692 standard; protein; 645 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2002; 2002WO-GB002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2001; 2001GB-00012687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium diphtheriae.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                            Best Local Similarity .... Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-167247/16.
                                                                                                           Sequence 645 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE35692;
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                                                                                                                                          Query Match
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infection and regularing nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating an neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for including prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct domprishing Corymebacterium diphtheriae diphtheria toxin translocation domain (Dip-HN domain) and botulinum type F neurotoxin from Clostridium botulinum. This sequence is used in the exemplification of the invention. (Updated on 23-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; HC; binding domain;
                                                                                                                                                                                                                                                                                                                                                                              1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                                                                                                                                                                                                                                                                                                                                                                                   61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
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   treating intracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKNTSSNGCFWSFISKEHGWOEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE35693 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium diphtheriae.
Clostridium botulinum.
Unidentified.
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                                                                                                                                                                                                                                                                                                                           Local Similarity
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The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells, preventing and reversing damage to cells, killing cells, promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for modulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including mascle spasms such as Dlephorospam, torticolis and
                                                                                                                                                                                                                                                                                                                                                                                                                      hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HW domain), botulinum type F neurotoxin binding domain (BONT/F-HC) from Clostridium botulinum and thrombin linker peptide. This sequence is used in the exemplification of the invention
                     Example 12; Page 60-63; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 657 AA;
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ö 574 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120 9 NI FSNTRLYTGVEVI IRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE Gaps ò Query Match 100.0%; Score 757; DB 6; Length 657; Best Local Similarity 100.0%; Pred. No. 3.1e-70; Matches 143; Conservative 0; Mismatches 0; Indels C RKNTSSNGCFWSFISKEHGWQEN 657 121 RKNTSSNGCFWSFISKEHGWOEN 143

BoNT/F-Hc-DipT HN domain-factor Xa linker fusion construct. AAE35694 standard; protein; 657 AA. 17-JUN-2003 (first entry) AAE35694; 

Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm; ODD9, Pronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; fusion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain; botulinum type F neurotoxin

21-MAY-2002; 2002WO-GB002384 WO200296467-A2 05-DEC-2002 Chimeric

Corynebacterium diphtheriae. Clostridium botulinum. Unidentified.

24-MAY-2001; 2001GB-00012687.

The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficking, for medulating expression of cell-surface markers and for inhibiting secretion from cells. The invention is also useful for treating prion disease, Alzheimer' disease and wide range of disorders in more constructions and incomparation and allocations and incomparation and incomparations and incomparations and incomparations and incomparations and incomparations and incomparations and incomparations and incomparations and incomparations and incomparations and incomparations are incomparations. hypersecretion disorders such as chronic obstructive pulmonary disease (COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheriat toxin translocation domain (DipT-HW domain). botulinum type F neurotoxin binding domain (BONT/F-HC) from Clostridium botulinum and factor Xa linker peptide. This sequence is used in the exemplification of the invention Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell. Example 12; Page 63-65; 130pp; English (MICR-) MICROBIOLOGICAL RES AUTHORITY. WPI; 2003-167247/16. Sequence 657 AA; Sutton JM, 

634 574 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE .. 0 100.0%; Score 757; DB 6; Length 657; 100.0%; Pred. No. 3.1e-70; 0; Mismatches RKNTSSNGCFWSFISKEHGWQEN 143 Query Match 100. Best Local Similarity 100. Matches 143; Conservative 61 121 셤 Š a ઠે ઠ

Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; botulinum neurotoxin type F; BONT/F. Modified clostridial heavy chain-superoxide dismutase conjugate #5 AAE07893 standard; protein; 685 AA 01-NOV-2001 (first entry) AAE07893; 635 RESULT 9

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WO200158936-A2 Synthetic Chimeric. 

Geobacillus stearothermophilus

Influenza virus. Clostridium botulinum.

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for delivering therapeutic colls including neurodespenzative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence or modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate compises bacterial Mn-superoxide dismutase (MnSOD), from Canjugate compisies absorbitus, linker that can be cleaved by factor Xa, translocation peptide from influenza virus and a neuronal cell-specific conjugate.
                                                                                                                                                                                                                                                                                           New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                 (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                              Example 9; Page 43; 50pp; English.
                                                                                                                                                                                                                 Silman N;
                                                          04-DEC-2000; 2000WO-GB004644.
                                                                                                         02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
                                                                                                                                                                                                              Sutton JM,
                                                                                                                                                                                                                                                     WPI; 2001-514643/56.
                                                                                                     02-DEC-1999;
                 16-AUG-2001
                                                                                                                                                                                                            Shone CC,
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Sequence 685 AA;

ö 61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTWNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 0; Gaps Length 685; 0; Indels Query Match
100.0%; Score 757; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.3e-70;
Matches 143; Conservative 0; Mismatches 0; RKNTSSNGCFWSFISKEHGWQEN 685 RKNTSSNGCFWSFISKEHGWOEN 143 603 121 663 g ઠ ઠે 셤 8 셤

AAE07890 standard; protein; 862 AA. (first entry) 01-NOV-2001 AAE07890; AAE07890 

Modified clostridial heavy chain-superoxide dismutase conjugate #2.

Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; botulinum neurotoxin type F; BONT/F.

The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain carboty terminal half of heavy chain (HC) of a neurotoxin, designated as HC that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocates the therapeutic agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin. Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to treat disorders of the CS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence conjudic clostridial heavy chain-superoxide dismutase conjudate. This conjugate comprises bacterial Mn-superoxide dismutase conjudate. This conjugate compliant, linker that can be cleaved by factor Xa, translocation domain from diphtheria neurotoxin and a neuronal cell. New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells. (MICR-) MICROBIOLOGICAL RES AUTHORITY. Example 9; Page 40; 50pp; English. Silman N; Geobacillus stearothermophilus, 02-DEC-1999; 99GB-00028530. 07-APR-2000; 2000GB-00008658. 04-DEC-2000; 2000WO-GB004644 Corynebacterium diphtheriae. Clostridium botulinum. Shone CC, Sutton JM, WPI; 2001-514643/56. WO200158936-A2 16-AUG-2001 Synthetic Chimeric. 

0; Gaps 0; Indels 100.0%; Score 757; DB 4; 100.0%; Pred. No. 4.4e-70; iive 0; Mismatches 0; Local Similarity 100. es 143; Conservative Sequence 862 AA; Query Match Best Loca Matches

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121 RKNTSSNGCFWSFISKEHGWQEN 143 AAE07892 standard; protein; 887 AA. 840 RKNTSSNGCFWSFISKEHGWOEN AAE07892; RESULT 11
AAE07892
ID AAE07
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AC AAE07
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DT 01-NO' g 셤 δ

01-NOV-2001 (first entry)

BoNT/F-Hc-DipT HN domain-factor Xa linker-YopT protein fusion construct

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AAE35713 standard; protein; 979

RESULT 12

17-JUN-2003 (first entry)

AAE35713;

Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer' disease; hypersecretion disorder; muscle spasm, COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; funion protein; diphtheria toxin; BONT/F; translocation domain; HN domain; DipT; Hc; binding domain; botulinum type F neurotoxin; targetted effector protien; YopT.

Corynebacterium diphtheriae. Clostridium botulinum.

Yersinia pestis. Unidentified.

Chimeric.

WO200296467-A2. 05-DEC-2002.

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of a HN domain of a clostridial toxin: Polypeptides of the invention are useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful to read disorders of the constructs are useful to treat disorders of the construct and infection. They are also useful in gene therapy. The present sequence is modified clostridial heavy chain-superoxide dismutase conjugate. This conjugate comprises a mitochondrial leader sequence from human Mn-superoxide dismutase (MnSOD), MnSOD from Bacillus stearothermophilus, linker that can be cleaved by thrombin, translocation domain from diphtheria neurotoxin and a neuronal cell-specific binding domain from botulinum neurotoxin type F (BONT/F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
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                                   Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; chimeric; superoxide dismutase; SOD; diphtheria neurotoxin; human; botulinum neurotoxin type F; BONT/F.
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  clostridial heavy chain-superoxide dismutase conjugate #4.
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100.0%; Pred. No. 4.6e-70;
ive 0; Mismatches 0;
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                                                                                                                                                       Geobacillus stearothermophilus.
Corynebacterium diphtheriae.
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nes 143; Conservative
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                                                                                                                                                                                               Clostridium botulinum.
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Matches
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(MICR-) MICROBIOLOGICAL RES AUTHORITY

Shone CC;

Sutton JM,

WPI; 2003-167247/16.

21-MAY-2002; 2002WO-GB002384 24-MAY-2001; 2001GB-00012687

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(COPD), bronchitis and asthma. The present sequence is a fusion construct comprising Corynebacterium diphtheriae diphtheria toxin translocation domain (DipT-HW domain), botulinum type F neurotoxin binding domain (BoNT/F-HO) from Clostridium botulinum and factor Xa linker peptide and Yersinia pestis targetred effector protien YopT. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a target cell. Pharmaceutical composition of the invention is useful for a treatment selected from promoting or inhibiting survival of cells; preventing and reversing damage to cells; killing cells; promoting or inhibiting the growth of cells, apoptosis, release of an inflammatory mediator from cells, division of cells and treating intracellular infection and regulating nitric oxide release from cells. The invention is useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular trafficients, for modulating expression of cell-surface markers and for trafficients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzheimer' disease and wide range of disorders including muscle spasms such as blephorospasm, torticolis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypersecretion disorders such as chronic obstructive pulmonary disease
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ö Length 979; Indels 100.0%; Score 757; DB 6; 100.0%; Pred. No. 5.2e-70; iive 0; Mismatches 0; Matches 143; Conservative Query Match Best Local Similarity

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61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI

1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPB 60

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The invention relates to a non toxic polypeptide, for delivery of a therapeutic agent to a neuronal cell, which comprises a binding domain (carboxy terminal half of heavy chain (HC) of a neurotoxin, designated as HC) that binds to the neuronal cell and a translocation domain (amino terminal half of HC, designated as HN), that translocation domain (amino agent into the neuronal cell, where the translocation domain is not a HN domain of a clostridial neurotoxin and is not a fragment or derivative of useful for the treatment of a disease state associated with neuronal cells. The polypeptide constructs are useful for delivering therapeutic substances to neuronal cells. They are useful for delivering therapeutic CNS including neurodegenerative diseases, stroke, epilepsy, brain tumours and infection. They are also useful in gene therapy. The present sequence is C. botulinum C2 enterotoxin translocation domain with botulinum controcation controcation to the exemplification of
                                                                       New non toxic polypeptide for delivery of a therapeutic agent for the treatment of a CNS disorder comprising a binding domain that translocates the therapeutic agent into the neuronal cells.
                                                                                                                                                                                                                                                                                                                                                                                  Neuronal cell; binding domain; translocation domain; stroke; epilepsy; tumour; infection; neurodegenerative disease; gene therapy; botulinum neurotoxin type F; BoNT/F.
                                                    KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                botulinum C2 translocation domain with BoNT/F-binding domain #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 757; DB 4; Length 1032; 100.0%; Pred. No. 5.5e-70; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                       RKNTSSNGCFWSFISKEHGWQEN 979
                                                                                                                        RKNTSSNGCFWSFISKEHGWOEN 143
                                                                                                                                                                                                                                         AAE07901 standard; protein; 1032 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 48; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1999; 99GB-00028530.
07-APR-2000; 2000GB-00008658.
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                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium botulinum
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950 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTWIRQNNNGGNIGLLGFHSNNLVASSWYYNNI 1009
                                                                                                                       120
The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn-SOD) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease and motor neurone diseases
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                                                                                                        61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A manganese superoxide dismutase (Mn-SOD) construct.
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                                                                                                                                                                                                                                                                                           1010 RKNTSSNGCFWSFISKEHGWQEN 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROBIOLOGICAL RES AUTHORITY.
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                                                                                                                                                                                                                                                         143
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                                                                                                                                                                                                                                                     121 RKNTSSNGCFWSFISKEHGWOEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93309 standard; protein; 1059
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Clostridium botulinum.
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Indels

100.0%; Score 757; DB 3; 1 100.0%; Pred. No. 5.7e-70; ive 0; Mismatches 0;

Best Local Similarity 100. Matches 143; Conservative

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1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE

Conservative

Similarity

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1 NIFSNITELYTGVEVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 

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                                  The present sequence represents a construct of the invention, comprising a mitochondrial leader sequence from human manganese superoxide dismutase (Mn-SOD), a Bacillus stearothermophilus Mn-SOD, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype F. The specification describes a composition for delivery of SOD to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a domain that translocates the SOD of the composition into the neuronal cell. After translocates the linker is cleaved to release the SOD. The composition is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and
                  61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia.
                                                                                                                                                                                                                                                                                                                                             Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1084;
                                                                                                                                                                                                                                                                                                                A manganese superoxide dismutase (Mn-SOD) construct.
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100.0%; Score 757; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.9e-70;
Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hallis B, Silman N;
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                                                                                                           1037 RKNTSSNGCFWSFISKEHGWQEN 1059
                                                                                     121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                             AAY93312 standard; protein; 1084 AA.
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Geobacillus stearothermophilus.
Clostridium botulinum.
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Job time: 68.5139 secs
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Indels

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

protein search, using sw model OM protein

Run on:

; Search time 11.9443 Seconds
(without alignments)
1151.928 Million cell updates/sec 2, 2006, 00:39:17 March

1 NIFSNTRLYTGVEVIIRKNG.......TSSNGCFWSFISKEHGWQEN 143 US-08-981-087B-4 757 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45

summaries

PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Ouery Match	Length	DB	ID	Description
-	607	80.2	1274	5	I40813	neurotoxin type F
8	581	76.8	1268	7	S33411	botulinum neurotox
m	401	53.0	1252	N	S21178	botulinum neurotox
4	374.5	49.5	1251	7	JH0256	botulinum neurotox
S	306.5	40.5	1296	Н	BTCLAB	bontoxilysin (EC 3
y	298.5	39.4	1296	~	I40645	botulinum neurotox
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12	107.5	14.2		~	A53878	type E neurotoxin
13	103.5	13.7		~	S11455	botulinum neurotox .
14	86	12.9		•	S71092	UV-damaged DNA bin
15	96.5	12.7		~	S14577	asparagine-rich pr
16	95	12.5		~	860538	envelope polyprote
17	91.5	12.1	_	7	S73786	hypothetical prote
18	91	12.0		~	T08605	
19	91	12.0		7	A64474	hypothetical prote
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C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C,Accession: I40813; S48108 C;Esst. M.D.; Roberts, T.A.; Thompson, D.E KESST, AK.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.E FENS Microbiol. Lett. 96, 225-230, 1992 A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum. A;Reference number: I40644

A, Accession: I40813

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA A;Residues: 1-1274 <RES> A;Cross-references: UNIPROT:P30996; UNIPARC:UPI0000126B8A; GB:M92906; NID:g144866; PIDN:

R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probbes for identification of the botulinal neurotoxin gene and specific id A;Title: aumber: \$48103; WUID:94013372; PMID:8408542
A;Accession: \$48108

Status: preliminary; translation not shown

A;Molecule type: DNA A;Residues: 634-1002 <CAM> A;Cross-references: UNIPARC:UP1000016EA7B; EMBL:X70816; NID:g407788; PIDN:CAA50147.1; PI C;Superfamily: tetanus toxin C;Keywords: neurotoxin

5 Gaps 4 Length 1274; Score 607; DB 2; Length 12 Pred. No. 1.9e-45; 8; Mismatches 12; Indels Ouery Match 80.2%; Best Local Similarity 83.1%; Matches 118; Conservative

9 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE ò 셤

KIIKLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120 ò

셤

RKNTSSNGCFWSFISKEHGWQE 142 121 ò 셤

# RESULT

- Clostridium barati botulinum neurotoxin type F - C;Species: Clostridium barati

C;Species: Clostridium barati C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004 C;Dates: 13-33411; S31860 R;Thompson, D.E.; Hutson, R.A.; Bast, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T FEMS Microbiol. Lett. 108, 175-182, 1993

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SCALING
Decidinal neurocoxin type E precursor - Clostridium botulinum
C, Species : Olostridium botulinum type-E murocoxin
C, Accession: S21179; MR 2017, MR 2017, MR 2017
M, Tiller The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin
A, Accession: S120 x WHES
A, Accession: S120 x WHES
A, Accession: S120 x WHES
A, Cross-references unber: S21178; MUID: 92174922; PMID: 1541280
A, Cross-references: UNIPPOT: 000496; UNIPPOT: Q4562; UNIPARC: UPIO000010A3; EMBL: X62683;
A, Cross-references: UNIPPOT: 000496; UNIPROT: Q4562; UNIPARC: UPIO000010A3; EMBL: X62683;
A, Cross-references: UNIPPOT: O011ins, M. D.; ESSET, A. K.
C, Clin Microbiol 31, 2255-222; MR 2017
A, Cross-references: UNIPRAC: UPIO00000C6F0; EMBL: X70815; NID: 940786; PIDN: CAASO146.1;
A, Accession: G49107
A, Accession: G49107
A, Accession: G49107
A, Accession: G404 acquence was submitted to the EMBL Data Library, January 1993
A, Accession: G404 acquence on the bound of the MR 2017
A, Nobec: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
A, Accession: G40527
A, Accession: G40527
A, Malle, M. Res. Comm. 133, 107-113, 1992
A, Accession: G40527
A, Malle, M. Res. Comm. 133, 107-113, 1992
A, Accession: G40527
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A, Accession: G40527
A, Accession: G
A,Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin A,Reference number: 833411, MUID:93252228; PMID:8486245
A,Rocession: 833411
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1268 <TMO>
A,Residues: 1-1268 <TMO>
C,Superfamily: tetanus toxin
C,Superfamily: tetanus toxin
C,Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1127 NIFSNARLYTGVEVIIRKVGSTDTSNTDNFVRKNDTVYINVVDGNSEYQLYADVSTSAVE 1186
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                                                                                                                                                                                                                                                                                                                                        Length 1268;
                                                                                                                                                                                                                                                                                                                                     76.8%; Score 581; DB 2; Length 12
76.8%; Pred. No. 3.7e-43;
ive 11; Mismatches 22; Indels
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Biochimie 72, 213-217, 1990
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  Matches 109;
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Best Local
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A; Molecule type: DNA
A; Residues: 1-27, E', 29-1251 <- POUD-
A; Residues: 1-27, E', 29-1251 <- POUD-
A; Residues: 1-27, E', 29-1251 <- POUD-
A; Cross-reneas: UNIPROT: P30995; UNIPARC: UPI000017670D; EMBL: X62088; NID: 940379
A; Experimental source: strains ATCC 43181 and ATCC 43755
B; Pujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N A; Pujii, N.; Kimura, S.; 199-255, 1991
A; Title: Oloning of a DNA fragment encoding the 5'-terminus of the botulinum type E tox A; Reference number: S16145; MUID: 91237316; PMID: 2033376
                                                                                                                          A; Molecule type: protein

A; Residues: 420-427 < CIMPA

A; Residues: 420-427 < CIMPA

A; Cross-references: UNIPARC: UPI0000176710

A; Experimental source: strain Beluga

A; Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin

C; Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit ne

C; Comment: The heavy chain mediates the binding of toxin to cell receptors while the li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiPoulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Bacchem. Biophys. Res. Commun. 183, 107-113, 1995
A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum typ.
A;Reference number: JH0256; MUID:92181428; PMID:1543481
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A;Cross-references: UNIPARC:UPT000016EA8F; EMBL:X53180; NID:g40407; PIDN:CAA37321.1; PI
A;Experimental source: strain BL6340
C;Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release
C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the li
A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the A;Reference number: A60027; MUID:90344918; PMID:2116911
A;Accession: A60027
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fil-422/Product: botulinum neurotoxin type E light chain #status predicted <LCH>F;423-1252/Product: botulinum neurotoxin type E heavy chain #status predicted <HCH>F;412-426/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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C;Species: Clostridium butyricum
C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 RLYTGVEVIIRK--NGSTDISNTDNFVRKNDLAXIN-VVDRDVEYRLYADISIAKPEKII
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llarity 54.7%; Pred. No. 5.8e-25;
Conservative 24; Mismatches 28
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A;Status: nucleic acid sequence not shown
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|TNSNGCFWNFISEEHGWOE 1251
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Best Local Similarity
Lag 76; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: neurotoxin
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A,Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associate C,Superfamily: tetanus toxin C;Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane prot E,2-444,Product: bontoxilysin A light chain #status experimental <LGHT> F;445-1256/Product: bontoxilysin A heavy chain #status experimental <HVY> F;223,227/Binding site: zinc (His) #status predicted F;224/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 1-1296 <RES>
Cross-references: UNIPROT:Q45894; UNIPARC:UPI000016EA88; EMBL:X73423; NID:g507070; PIC
                                                                                                                                                                                                                                                                                                                                                                                                                                  Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium botulinum type
                                                                                                                                                                                                                             E.; Suedhof, T.C.; Jahn,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      botulinum neurotoxin type A - Clostridium botulinum
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140645
B;Willems, A.; East, A.K.; Lawson, P.A.; Collins, M.D.
Res. Microbiol. 144, 547-556, 1993
A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botul
A;Reference number: I40645; MUID:94143603; PMID:8310180
Partial sequence of the light chain of botulinum neurotoxin type A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV
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                                                                                                                                                                                    A,Cross-references: UNIPARC:UP10000173659
R,Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteclysis of SNAP-25 by types E and A botulinal neurotoxins.
A,Reference number: A49708; MUID:94124495; PMID:8294407
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Pred. No. 3e-18;
2; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.5%; Score 306.5; DB 1;
Best Local Similarity 44.4%; Pred. No. 6e-19;
Matches 67; Conservative 21; Mismatches 50;
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43.4%; Pre-
tive 22;
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                                             ence number: A27000
                                                                                                                      Molecule type: protein :Residues: 2-47 <DAS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 66; Conserv
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                                                                                 Accession: A27000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: atx; botA
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A; Residues: 1-1256 <BIN>
A; Residues: 1-1256 <BIN>
A; Cross-references: UNIPROT: P10845; UNIPARC: UPI0000001386; GB: M30196; NID: G144864; PIDN:
A; Experimental source: strain 62A, subtype A
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
R; Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.; Atkinson, T.
Br. J. Blochem: 189, 73-81, 1990
A; Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin
A; Reference number: S09492; MUID: 90235864; PMID: 2185020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after expanding the perfect of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NiAlternate names: botulinum neurotoxin type A
C;Species: Clostridium botulinum
C;Species: al-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A35294; S69492; S68220; A33401; A53884; A60025; A27000
R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
J Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other A;Reference number: A35294; MuID:90264400; PMID:2160960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1, 0, 3-26, VV, 28-1296 <THO>
Cross-references: UNIPARC:UPI000003409D; EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID
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                                                                                              KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN 123
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Residues: 867-880;1148-1217,'Y',1219 <GIM>
Cross-references: UNIPARC:UP100000BBB24; UNIPARC:UP1000173656
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A; Residues: 2-6;445-453, X7,455-457 <DAS1>
A; Cross-references: UNIPARC:UP10000173657; UNIPARC:UP10000173658
R; DasGupta, B.R.; Foley, J.; Niece, R.
Biochemistry 26, 4162, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bontoxilysin (EC 3.4.24.69) A precursor - Clostridium botulinum
                                                                                                                                                                                                                                                     1232 TNSNGFFWNFISEEHGWQE 1250
                                                                                                                                                                                                        124 ISSNGCFWSFISKEHGWQE 142
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A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-313,'S',315-451 <KUR>
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Molecule type: protein
Residues: 2-16 <SCH1>
preliminary
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A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: 1-1291 cRES>
A/Status: 1-1291 cRES>
A/Status: 1-1291 cRES>
A/Cross-references: UNIPROT.Q08077; UNIPARC:UP100000BDC86; EMBL:X71343; NID:g296148; PID
B/Campbell, K.D.; Collins, M.D.; East, A.K.
A/Title: Gene probes for identification of the botulinal neurotoxin gene and specific id
A/Reference number: S48103; MUID:94013372; PMID:8408542
                                                                                                                                                                                C)Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 09-Jul-2004
C(Accession: I40631; S48103; $48104; $36015
R;Hutson, R.A.; Collins, M.D.; Bast, A.K.; Thompson, D.E.
Curr. Microbiol. 28, 101-110, 1984
A;Tttle: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinu
A;Reference number: 140631; MUID:94122659; PMID:7764370
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A48940

Dontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum

N.Alternate names: botulinum neuvotoxin type B (BoNT/B)

C,Species: Clostridium botulinum

C,Species: Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

C,Accession: A48940; 88105; E31575; A82871; 801155; 808562; 807128; 808573; 808574

R,Whelan, S.M.; Blmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.

A)Ppl. Environ: Microbiol. 58, 2345-2354, 1992;

A)Title: Molecular cloning of the Clostridium botulinum structural gene encoding the typ

A;Reference number: A48940; MUID:92384550; PMID:1514783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 634-843, 'T', 845,'N', 847-994 <CAMZ>
A; Estidues: 634-843, 'T', 845,'N', 847-994 <CAMZ>
A; Cross-references: UNIPARC: UPIO0000B7A6E; EMBL: X70819; NID: 9407780; PIDN: CAA50150.1; E
A; Experimental source: non-proteolytic strain Eklund 2B (Colworth 229)
C; Comment: Botulinum neurotoxin type B in these strains may posses a capable catalytic
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Modecule type: DNA
A; Residues: 634-761, E', 763-841, M', 843, T', 845, N', 847-994 <CAMI>
A; Residues: 634-761, E', 763-841, M', 843, T', 845, N', 847-994 <CAMI>
A; Cross-references: UNIPARC: UPI00000BEAEF; EMBL: X70814; NID: 9407778; PIDN: CAAS0145.1;
A; Experimental source: non-proteolytic strain 2129B (Scott)
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: tetanus toxin
(Superfamily: tetanus toxin
(Staywords metalloprotein; neurotoxin; transmembrane protein; zinc
(1244/Product: botulinum neurotoxin type B light chain #status predicted <LGHT>
(1442-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HVY>
(1230,234/Binding site: zinc (His) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary, nucleic acid sequence not shown; translation not shown
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21.1%; Score 160; DB 2;
Best Local Similarity 29.2%; Pred. No. 4.8e-06;
Matches 47; Conservative 28; Mismatches 66;
                                                                                                                                                           Species: Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 634-994 «CAM»
A;Experimental source: proteolytic type B, strain NCTC 7273
A;Experimental source: proteolytic type B, strain NCTC 7273
A;Experimental source: proteolytic type B, strain NCTC 7273
A;Experimental source: proteolytic type B, strain NCTC 7273
A;Bestabo: Ex.; Pemberton, J.M.; Desmarchelier, P.M.
A;Description: Partial amino acid sequence of botulinum neurotoxin type B and comparisic
A;Accession: S1575
A;Molecule type: DNA
A;Rosidues: 36-217, G',219-224,'S',226-246 «SZA»
A;Cross-references: UNIPARC:UP1000016EA79; EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PIC
B;Kurazono, H; Mochida, S; Binz, T; Bisel, U; Quanz, M; Grebenstein, O.; Wernars, K
J. Biol. Chem. 267, 14721-14729, 1992
A;Title: Minimal essential domains specifying toxicity of the light chains of tetanus to
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 2-17 < kSCH2.
A; Accession: S08574
A; Accession: S08574
A; Accession: S08574
A; Molecule type: protein
A; Residues: preliminary
A; Molecule type: protein
A; Residues: 442-459
A; Corser-references: UNIPARC: UPI0000173652
B; Coniavo, G; Benfenati, F; Poulain, B; Rossetto, O; de Laureto, P.P.; DasGupta, B.R.
A; Coniavo, G; Benfenati, F; Poulain, B; Rossetto, O; de Laureto, P.P.; DasGupta, B.R.
A; Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyti
A; Residues: 1-121 (MHE)
A; Cross-references: UNIPROT: P10844; UNIPARC: UP1000016EA76; GB: M81186; NID: g144734; PIDN
A; Cross-references: UNIPROT: P10844; UNIPARC: UP1000016EA76; GB: M81186; NID: g144734; PIDN
A; Experimental source: type B, Danish
A; Campbell, K.D.; Collins, M.D.; East, A.K.
A; Campbell, K.D.; Collins, M.D.; East, A.K.
A; Title: Gene probes for identification of the botulinal neurotoxin gene and specific in A; A; Reference number: S48103; MUID: 94013372; PMID: 8408542
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A.Sxperimental source: strain Okra
A.Note: sequence extracted from NCBI backbone (NCBIP:109365)
B.Dastupta, B.R.; Datta, A.
B.Jochimie 70, 811-817, 1989
A.TILLIB: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with A.Reference number: S07155; MUID:89000987; PMID:3139097
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C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synaps
C;Genetics:
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A/Residues: 2-29, /m',31-45 <DAS>
A/Accession: 508562
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;Molecule type: DNA
;Residues: 1-1315 <EIS>
;Cross-references: UNIPROT:P04958; UNIPARC:UP100003617E; GB:X04436; NID:g40769; PIDN:C.
                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1315 < PAL>
A; Residues: 1-1315 < PAL>
A; Residues: 1-1315 < PAL>
A; Cross-references: UNIPARC: UPI000003617E; GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g
A; Experimental source: strain CN3911
A; Experimental source: strain CN3911
B; Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
A; Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in E
A; Reference number: A25194; MUID:86085672; PMID:3510187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,Molecule type: DNA
1,Residues: 743-1315 <PA2>
1,Cross-references: UNIPARC:UPI0000156CFA; GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:
1,Accession: B25194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, nfect. Immun. 57, 3588-3593, 1989
'Title: Isolation, purification, and characterization of fra Reference number: A60759; WUID:90035436; PMID:2478476
                                                                                                              R;Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A;Title: The complete nucleotide sequence of tetanus toxin.
A;Reference number: A25757; MUID:87040747; PMID:3774547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 865-894 <FA3>
A;Cross-references: UNIPARC:UP1000017364D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 461-475 <MAT>
A;Cross-references: UNIPARC:UP1000017364E
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Best Local Similarity 23.4%;
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A;Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botu
A;Reference number: A25689; MUID:87053814; PMID:3536478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurocoxin - Clostridium botulinum

neurocoxin - Clostridium botulinum

C;Species Clostridium botulinum

C;Species Clostridium botulinum

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C;Superfamily: Letanus

C;Superfamily: tetanus coxin

C;Superfamily: tetanus coxin

C;Superfamily: tetanus coxin
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N'Alternate names: tetanus neurotoxin
C;Species: Clostridium tetani
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
R;Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, EMBO J. 5, 2495-2502, 1986
A;Gene: bont/b
C;Function:
A;Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2
A;Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2
C;Superfamily: tetanus toxin
C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F;2-441/Product: bontoxilysin B light chain #status experimental cLGHT>
F;42-1291/Product: bontoxilysin B heavy chain #status experimental cHVY>
F;230,234/Binding site: zinc (His) #status predicted
F;231/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FSNT-----RLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVD-RDVEYRLYADISI
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                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                            Length 1291;
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                                                                                                                                                                                                                                                                                                                                                   65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TSNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH---
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                                                                                                                                                                                                                                                                                            ; Score 149; DB 1;
; Pred. No. 4.5e-05;
28; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.8%; Score 142.5; DB 2
25.6%; Pred. No. 0.00017;
iive 25; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 VASSWYYNNIRKN--TSSNGCFWSFISKEHGWQE 142
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26.6%;
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nes 41; Conservative
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Matches 42; Conserv
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B, the NH-2-terminal

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R;Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G. J. Immunol. 142, 394-402, 1989
A;Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A;Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A;Contents: annotation; epitope region
R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt A;Reference number: S27125; MUID:93063293; PMID:1331807
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: The source of this protein was an extrachromosomal plasmid.
C;Comment: The precursor is cleaved by endogenous proteinase activity to form light (fra Gual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C;Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to ganglio C;Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt C;Superfamily: tetanus toxin C;Superfamily: tetanus toxin c;Superfamily: transmembrane protein; zinc c;Superfamily: tetanus metalloproteinase; neurotoxin; transmembrane protein; zinc F;2-457/Product: tentoxylysin light chain (fragment A) #status predicted <TTL> F;461-1315/Product: tentoxylysin heavy chain (fragment B.C) #status experimental <TTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ride Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C. Eur. J. Biochem. 229, 61-69, 1995
A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin A;Reference number: S69348; MUID:95262688; PMID:7744050
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F;234/Active site: Glu #status predicted
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47; Indels

	1312 RESULT 13 S11455 Botulinum neurotoxin type D - Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium botulinum C;Species: Clostridium C;Species: Clostridium C;Accession: S11455 Nuclect Acids Res. 18, 5556, 1990 A;Tile: Nucleotide sequence of the gene encoding Clostridium A;Accession: S11455 A;Stus: preliminary; translation not shown A;Accession: S11455 A;Ctus: preliminary; translation not shown A;Molecule type: DNA A;Ctus: preliminary; translation not shown A;Ctoss-references: UNIPROT:P19321; UNIPARC:UPI0000126B83; EMI C;Superfamily: tetanus toxin C;Keywords: neurotoxin C;Keywords: neurotoxin C;Keywords: neurotoxin		RESULT 12 Cype Enginements) Cype Construction botulinum (fragments) Cype Construction botulinum (fragments) Cype Construction and Cype Construction botulinum (fragments) Cype Construction Cype Construction Cype Construction 18-Nov-1994 #text_change 11-Dec-2004 Cybec Construction Cype Cype Construction Cype Cype Cype Cype Cype Cype Cype Cype
	RESULT 11 T09057 Probable protein-histidine kinas NyAlternate names: histidine kinas CiSpecies: Dictyostelium discoid CiAccession: T1-Jun-1999 #sequence_re CiAccession: T09057 RiSingleton, C.K.; Mykytka, B.; submitted to the EMBL Data Libra A; Reference number: 216542 A; Reference number: 216542 A; Residues: Preliminary; translates A; Residues: 1-1225 <sin> C; Genetics: A; Gene: dhkC</sin>	A; Map position: 4 C; Keywords: phosphotransferase; prote Query Match Best Local Similarity 30.1%; Pre Matches 43; Conservative 18; Pre Matches 5 NTRLYTGVEVIIRANGS:	RESULT 12 A5.878 Lype E neurotoxin - Clostridium bc Lype E neurotoxin - Clostridium bc Lype E neurotoxin - Clostridium bc Lybe E neurotoxin - Clostridium bc Lybecesion: A5.878 Rydimenaz, J.A.; DasGupta, B.R. Rydimenaz, J.A.; DasGupta, B.R. A;Title: Pepsin fragmentation of PA;Reference number: A5.878; MUID:9 A;Reference number: A5.878; MUID:9 A;Contents: Lype E, E-43, Alaska A;Contents: Lype E, E-43, Alaska A;Molecule Lype: protein A;Residues: 1-122 clim> A;Residues: 1-122 clim> A;Residues: 1-122 clim> A;Rocoss-references: UNIPROT: Q9R5H0 A;Note: sequence extracted from NC C;Keywords: neurotoxin Query Match Best Local Similarity 45.3%; Matches 28; Conservative 9

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asparagine-rich protein (clone 14C1) - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: 20-Feb-1995 #text_change 09-Jul-2004 C;Accession: 814577 F;Schreiber, L.; Deutsche, U.; Storck, T.; Mueller-Hill, D. submitted to the EMBL Data Library, December 1989 A;Reference number: $14469
                                                                                                                                                                                                                             66 IRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNN----IR 121
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                                                                                                                                     9 YTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRD---VEYRLYADISIAKPEKIIKL
                                                                                          Gaps
                                          12.9%; Score 98; DB 2; Length 1139; larity 28.0%; Pred. No. 1.2; Conservative 21; Mismatches 41; Indels :
C; Superfamily: UV-damaged DNA-binding protein
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Best Local Similarity
Matches 35; Conserv
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A;Accession: S14577 A;Status: preliminary A;Molecule type: mRNA A;Reducus: 1-391 «SGCI» A;Cross-references: UNIPROT:Q25768; UNIPARC:UPI000080C7F; EMBL:X17483; NID:g9842; PID:g

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1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60

; Score 96.5; DB 2; Length 391; ; Pred. No. 0.47; 33; Mismatches 55; Indels 17; Gaps

Query Match 12.7%; Best Local Similarity 22.8%; Matches 31; Conservative 3 103 KDCFDILNNQMRSENLKNVLKDVLKMNTPGSTMTNNYHMNIKENNGTTLR----DSHHYV 158

112 ASSWYYNNIRKNTSSN 127 | : | | | : | 159 TTTTNNNNNNNNNNN 174 2, 2006, 00:47:44

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# ALIGNMENTS

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Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.
R Elmore M.J., Boddworth N.J., Whelan S.M., Minton N.P.;
Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.
R EMBL; X81714; CAA57386.1; -; Genomic_DNA.
R EMBL; L35496; AAA2310.1; -; Genomic_DNA.
R EMBL; ASSP, Q45894; 1EIH.
R MEROPS; M.27.002; -: Genomic_DNA.
R GO; GO:0016021; F:metallopeptidase activity; IEA.
R GO; GO:0016021; F:metallopeptidase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001591; Botulinum.
R InterPro; IPR001591; Botulinum.
InterPro; IPR001591; Peptidase M.7.
R PFAMT; PR01742; Peptidase M.7.
R PRINTS; PR00760; BONTOXILYSIN.
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                               Last sequence update)
Last annotation update)
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100.0%; Pred. No. 7.2e-58;
iive 0; Mismatches 0;
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Neurotoxin.
                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-REB-2005 (TrEMBLrel. 09, Last ann
BONT/F (Neurotoxin type F).
Name=bont/f; Synonyms=bonT/F;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Cl
                                                      Created)
057236 CLOBO PRELIMINARY;
057236; 045863;
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1256 RKNTSSNGCFWSFISKEHGWQEN 1278

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MEDLINE=88440323; PubMed=9767710; DOI=10.1007/s002849900384;
Santos-Buelga J., Collins M.D., East A.K.;
"Characterization of the genes encoding the Botulinum neurotoxin complex in a strain of clostridium botulinum producing type B & Fneurotoxins.";
                                                                                                                                          Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1491;
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01-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annocation update)
Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BoNT/F)
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 84.4%; Score 639; DB 2; Length 12 Best Local Similarity 84.5%; Pred. No. 1.9e-47; Matches 120; Conservative 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1280 AA; 147486 MW; D0F748976EBC222C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Santos-Buelga J.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y13631; CAA73972.1; -; Genomic_DNA.
HSSP; Q45894; 1E1H.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008455; F:metallopeptidase activity; IEA.
GO; GO:0006508; P:pathogenesis; IEA.
InterPro; IPR011591; Botulinum.
InterPro; IPR0000395; Peptidase M27.
InterPro; IPR0005035; Peptidase M27.
InterPro; IPR006025; Peptidase M27.
PFam; PF01742; Peptidase M27; I.
PRINTS; PR00760; BONTOXITYSIN.
                                                                Created)
Last sequence update)
Last annotation update)
                                    1280 AA
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                                    PRT;
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                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAK-2004 (TrEMBLrel. 26,
                               Q9ZAJS CLOBO PRELIMINARY;
Q9ZAJS;
                                                              01-MAY-1999 (TrEMBLrel.
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STRAIN=CDC 3281;
                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                  BonT protein.
                                                                                                                                Name=bonT;
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P30996;
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RA Fadurasaki S., Baumeister A., Binar T., Blasi J., Link E., Cornille F., Ranasaki S., Baumeister A., Binar T., Blasi J., Link E., Cornille F., Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.; T., Clavage of members of the synaptobrevin/VAMP family by types D and F T. Clavage of members of the synaptobrevin/VAMP family by types D and F Biol. Chem. 269:12764-12772(1994).

The Dotulinal neurotoxins and tetanus toxin. T. FOWCTION: Botulinum foxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where I can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc. CATALYTIC ACTIVITY: Limited hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of the S8-Gln-|-Lys-S9 condopeptidase that catalyzes the hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevine, SNAP25 or syntaxin. No condopeptidase that catalyzes the hydrolysis of condopeptidase that catalyzes the hydrolysis of proteins of the heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel community that the N- and C-terminal of the heavy chain mediate channel community. The submitment of a light chain mediate channel community that the N- and C-terminal of the heavy chain (H). The Light chain mediate channel community that the N- and C-terminal of the heavy chain (H). The Light chain mediate channel co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      East A.K., Collins M.D., "Conserved structure of genes encoding components of botulinum neurotoxin complex M and the sequence of the gene coding for the nontoxic component in nonproteclytic Clostridium botulinum type F.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94013372; PubMed=8408542; Cambbell K.D., Collins M.D., East A.K.; Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                             East A.K., Richardson P.T., Allaway D., Collins M.D., Roberts T.A., Thompson D.E.;
                                                                                                                                                                                                         STRAIN=TYPE F / ATCC 23387;
MEDLINE=93012902; PubMed=1398040; DOI=10.1016/0378-1097(92)90408-G;
                                                                            Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                             "Sequence of the gene encoding type F neurotoxin of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M92906; AAA23263.1; -; Genomic_DNA.
EMBL; 873676; AAC60475.1; -; Genomic_DNA.
EMBL; X70820; CAA50151.1; -; Genomic_DNA.
EMBL; X70816; CAA50147.1; -; Genomic_DNA.
PIR; 140813; 140813.
PIR; 548109; 548109.
MESCP ; Q4894; 1E1H.
                                                                                                                                                                                                                                                                                                                                                                    FEMS Microbiol. Lett. 75:225-230(1992).
Botulinum neurotoxin F heavy chain]
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STRAIN-TYPE F / Hobbs FT10;
MEDLINE-94297488; PubMed=7764998;
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IDENTIFICATION OF SUBSTRATE.
                                                                                                                                                                                   SEQUENCE.
                                                   Clostridium botulinum.
                                                                                                                               NCBI_TaxID=1491;
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ProDom; PD001963; Botulinum; 1. PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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EMBL; AB037713; BAB03521.1
EMBL; AB037711; BAB03519.1
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EMBL; AB037709; BAB03516.1
EMBL; AB037707; BAB03515.1
HSSP; Q45894; 1E1H.
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Q9K395;
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                           Neurotoxin.
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EMBL; X66262; CAA48329.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
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                                                                                                                                                             1274 Ab; 146710 MW; 5899756A74388921 CRC64;
                                   InterPro; IPR012929; Toxin_trans.
InterPro; IPR012920; Toxin_trans.
Pfam; PF01451; Deptidase MZ7; 1.
Pfam; PF07952; Toxin_trans; 1.
PRINTS; PR00766; BONTOXILXSIN.
ProDom; PR001963; BOCTULIANIN. 1.
PRODOM; PS00142; ZINC PROTEASE; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                             Score 607; DB·1; Length 1274;
Pred. No. 1.2e-44;
8; Mismatches 12; Indels
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GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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InterPro; IPRO00395; Peptidase M27.
InterPro; IPRO06025; Pept M Zn BS.
Pfam; PP01742; Peptidase M27; I.
                 Pept M Zn BS.
Peptidase_M27
     Botulinum
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Best Local Similarity 83.1%;
Matches 118; Conservative
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                                                                                                                                                       Toxin; Transmembrane; Zinc.
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Q45851 9CLOT PRELIMINARY;
Q45851;
                  InterPro; IPR006025;
InterPro; IPR000395;
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61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                                                                                                        1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                  Length 1268;
                                                                                                        22; Indels
963040091AC15ED2 CRC64;
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GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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Last sequence update)
Last annotation update)
                                                  Query Match 76.8%; Score 581; DB 2; Best Local Similarity 76.8%; Pred. No. 2.4e-42; Matches 109; Conservative 11; Mismatches 22
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR012928; Toxin_reap. Dd_N.
InterPro; IPR012928; Toxin_reap. Dd_N.
Pfam; PF07953; Toxin_R. Dind N; 1.
Pfam; PF07952; Toxin_R. Dind N; 1.
PRINTS; PR00760; BONTOXILYSIN.
PRODOM; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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EMBL, AB037714; BAB03522.1; -; Genomic_DNA.

EMBL, AB037704; BAB03512.1; -; Genomic_DNA.

EMBL, AB037705; BAB03513.1; -; Genomic_DNA.

EMBL, AB037706; BAB03513.1; -; Genomic_DNA.

EMBL, AB037710; BAB03518.1; -; Genomic_DNA.

EMBL, AB037710; BAB03518.1; -; Genomic_DNA.
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MEDLINE=20509829; PubMed=11055954;
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     1268 AA; 145512 MW;
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TNSNGFFWNFISEEHGWQE 1251
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Q9FAR6;
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                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1492;
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                                                                                        7 RLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLI 66
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Type B botulinum toxin.
Name=bont/E;
Name=bont/E;
10stridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TAXID=1492;
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Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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TBukamoto K., Mukamoto M., Kohda T., Ihara H., Wang X., Maegawa Nakamura S., Karasawa T., Kozaki S.;
"Sequence of the borulinum neurotoxin type E.";
"Submitted (MAR-2002) to the EMBL/Genbank/DDBJ databases.
EMBL; AB082519; BAB86845.1; -; Genomic_DNA.
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                                Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1252;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Indels
 1251 AA; 143752 MW; 2021F4E427070296 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1252 AA; 143637 MW; 76401D4D2E95D7A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                   13-5EP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Botulinum neurotoxin type E.
                                                             31;
                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.0%; Score 401; DB 2;
55.4%; Pred. No. 1.8e-26;
iive 26; Mismatches 26
                              55.2%; Score 417.5; DB 2 55.9%; Pred. No. 6.3e-28;
                                                                                                                                                                                                                                                                                                                           PRT; 1252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1252 AA.
                                                             24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1233 TNSNGCFWNFISEEHGWOE 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 TSSNGCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                 1235 NGCFWNFISEEHGWQE 1250
                                                                                                                                                                                                                127 NGCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                                                                                                       Q54A79_CLOBO PRELIMINARY;
Q54A79;
                                           Best Local Similarity 55.9
Matches 76, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.4
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBKZM3_CLOBU PRELIMINARY;
Q8KZM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                 Name=bont/E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium.
SEQUENCE
                              Query Match
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1120 RLYSGIKVKIQRVNNSSTN----DNLVRKNDQVYINFVASKTHLLPLYADTATTNKEKTI 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 KLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN
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MEDLINE=20509829; PubMed=11055954;

MEDLINE=20509829; PubMed=11055954;

DOI=10.1128/AEM.66.11.4992-4997.2000;

Wang X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Y., Yamakawa K., Oguma K., Sakkayachi Y., Nakamura S.;

"Genetic analysis of type E botulinum toxin-producing Clostridium butyricum strains.";

"Appl. Environ. Microbiol. 66:4992-4997(2000).

EMBL; AB039264; BAB12249.1; -; Genomic_DNA.
STRAIN=BL 5262;
Taylamoto M., Kohda T., Ihara H., Wang X., Maegawa T.,
Nakamura S., Karaswa T., Kozaki S.;
Submitred (JUL-2002) to the EMBL/GenBank/DDBJ databases.
Bmbl, ABO88207; BACG5434.1; -; Genomic_DNA.
HSSP; Q45894; LEIH.
SWR; Q6KZM3; 2-412.
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Clostridium.
                                                                                                                                                     GO; GO:000827; F:metallopeptidase activity; IEA.
GO; GO:000827; F:metallopeptidase activity; IEA.
GO; GO:0008297; F:metallopeptidase activity; IEA.
GO; GO:0008208; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001591; Botulinum.
R InterPro; IPR000395; Peptidase M27.
InterPro; IPR000395; Peptidase M27.
R Pfam; PF01742; Peptidase M27; I.
R PRINTS; PR00760; BONTOXIIVSIN.
R PFODOm; PD001963; BOtulinum; 1.
R PROSITE; PS00142; ZINC PROTEARS; UNKNOWN 1.
S PROSITE; PS00142; ZINC PROTEARS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1252;
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GO; GC:0008237; F:metallopeptidase activity; IEA.
GO; GO:0009405; F:pathogenesis; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR0011591; Botulinum.
InterPro; IPR0001595; Peptidase M27.
InterPro; IPR0001595; Peptidase M27.
Pfam; PF01742; Peptidase_M27; I.
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Last sequence update)
Last annotation update)
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Best Local Similarity 55.4%; Pred. No. 1.4e-25;
Matches 77; Conservative 24; Mismatches 28;
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Biochimie 72:213-217(1990).
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Gimenez J.A., Dasgupta B.R.; "Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the site trypsin nicks and homology with tetanus neurotoxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92174922; PubMed=1541280; Whelan S.M., almore M.J., Boddworth N.J., Atkinson T., Minton N.P.; Whelan S.M., almore M.J., Boddworth N.J., Atkinson T., Minton N.P.; "The complete amino acid sequence of the Clostridium botuliuum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding
                                                                                                                                           KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN
                                                                                                7 RLYTGVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLEOTIDE SEQUENCE OF 1-251.
MEDLINE=90264400; PubMed=2160960;
Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
J. Biol. Chem. 265:9153-9158(1990).
                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                        Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEQUENCE OF 419-426.
MEDLINE=90344918; Pubmed=2116911; DOI=10.1016/0300-9084(90)90075-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-85197963; Pubmed-1888113; Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.; Rathyamoorthy V., Masgupta B.R.; Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                                                                                                                                                                                                                 Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                         10;
                                                      Length 1255;
                                                      51.7%; Score 391; DB 2; Length 12
55.4%; Pred. No. 1.4e-25;
ive 24; Mismatches 28; Indels
            Prodom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 1255 AA; 143917 MW; 1B557B9D85CD8E4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 183:107-113(1992)
                                                                                                                                                                                                                                                                 1250 AA
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                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                            Botulinum neurotoxin E heavy chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.";
Bur. J. Biochem. 204:657-667(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Type E / Beluga;
MEDLINE=92181428; PubMed=1543481;
                                                                                                                                                                                                  1236 |:||| ||:|||:|||||||
1236 TNSNGFFWNFISEEHGWQE 1254
                                                                                                                                                                                      124 TSSNGCFWSFISKEHGWOE 142
   BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 1-13.
                                                                  Local Similarity 55.4 tes 77; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1491;
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                                                      Query Match
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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J. Biol. Chem. 269:1617-1620(1994).
-!- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsyraptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptiadae that catalyzes the hydrolysis of the 180-Arg-|-Ile-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 bond in SNAP-25.
CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates to syntaxin. No COPACTOR: Binds 1 zinc ion per subunit (By similarity).
SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94124495; PubMed-8294407;
Binz T., Blasi J., Yamagaki S., Baumeister A., Link E., Suedhof T.C.,
Jahn R., Niemann H.;
                                                                                                                              neurotoxin gene and
                                                                                                                                                                                                                                                                                                                         MEDLINE=94063091; PubMed=8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.; Bottenati F., Wilson M.C., Montecucco C.; Bottenina neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0766; BONTOXILYSIN.
PRODOM; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Metalloprotease; Neurotoxin; Protease; Toxin; Transmembrane; Zinc. INIT_MET
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STRAIN=Type E / Hazen 36208;
MEDLINE=94013372; PubMed=8408542;
Campbell K.D., Collins M.D., East A.K.;
"Gene probes for identification of the botulinal neurotoxir specific identification of neurotoxin types B, E, and F.";
J. Clin. Microbiol. 31:2255-2262(1993).
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EMBL, X62683; CAA44558.1; -; Genomic_DNA.
EMBL, X70815; CAA50146.1; -; Genomic_DNA.
PIR, S208575; S08575.
PIR, S21178; S21178.
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InterPro; IPR000395; Peptidase M27.
InterPro; IPR012928; Toxin recpt bd N.
InterPro; IPR012500; Toxin trans.
Pfam; PF01742; Peptidase M27; 1.
Pfam; PF07953; Toxin R bind N; 1.
Pfam; PF07952; Toxin trans: 1.
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PDB; 1T3C; X-ray; A/B=1-421.
                                                                                                                                                                                                                                                                                                    IDENTIFICATION OF SUBSTRATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lett. 335:99-103(1993)
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MEROPS; M27.002
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64 KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gimens J., Foley J., Dasgupta B.R.,
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
"Neurotoxin type E from Clostridium botulinum and C. butyricum;
partial sequence and comparison.",
PASEB J. 2.A1750-A1750
                                                                                                                                                                                                                                                                                           7 RLYTGVEVIIRK--NGSTDISNTDNFVRKNDLAYIN-VVDRDVEYRLYADISIAKPEKII
                                                                                                                                                                                                                              Query Match 50.8%; Score 384.5; DB 1; Length 1250; Best Local Similarity 54.7%; Pred. No. 5.2e-25; Matches 76; Conservative 26; Mismatches 26; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91237316; PubMed=2033376; Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K., Yokosawa N., Yashiki T., Oguma K.; "Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340."; J. Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WUCLEOTIDE SEQUENCE.
STRAIN=ATCC 43181, and ATCC 43755;
MEDLINE=92181428; bubMed=1543481;
MEDLINE=92181428; bubMed=1543481;
Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
"Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 4475).";
Biochem. Biophys. Res. Commun. 183:107-113(1992).
            By similarity.

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Interchain (between light and heavy chains) (Probable).

R - G (in Ref. 2).

C - S (in Ref. 2).

I -> L (in Ref. 2).

I -> LO (in Ref. 2 and 6).

FE -> LO (in Ref. 2 and 6).

FR -> A (in Ref. 2 and 6).

R -> A (in Ref. 2 and 6).

R -> A (in Ref. 2 and 6).

R -> N (in Ref. 2 and 6).

R -> N (in Ref. 2 and 6).

R -> N (in Ref. 2).
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01-071-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BONT/E)
(Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain,
Electridium butyricum.
Bacteria, Pirmicutes; Clostridia, Clostridiales, Clostridiaceae;
   Botulinum neurotoxin E heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1250 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    124 TSSNGCFWSFISKEHGWQE 142
                                                                                                                                                                                                    143713 MW;
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P30995;
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InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR0060395; Pept M Zn BS.

InterPro; IPR012500; Toxin recpt bd_N.

InterPro; IPR012500; Toxin treapt bd_N.

InterPro; IPR012500; Toxin trans.

IN Pfam; PF07953; Toxin trans.

IN PR0096; DF001960; BONTOXILYSIN.

INTERPROSE PR00142; INC PR0TEASE; I.

INTERPROSE PR00142; ZINC PROTEASE; I.

INTERPROSE PROTECT PROTEASE; I.

INTERPROSE PROTECT PROTEASE; I.

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and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc
                                                                          endopeptidase.
-!-CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevius, SNAP25 or syntaxin. No detected action on small molecule substrates.
-!-COFACTOR: Binds 1 zinc ion per subunit (By similarity)
-!-SUBRUIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.
-!-SUBCELLULAR LOCATION: Serreted.
-!-MISCELLANBOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.
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211 211 Zinc (catalytic) (By similarity).
215 Zinc (catalytic) (By similarity).
411 425 Interchain (between light and heavy chains) (Probable).
229 229 K -> M (in Ref. 2).
1250 AA; 143266 MW; 8171B5B2C2312857 CRC64;
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EMBL; X53180; CAA37321.1; -; Genomic_DNA.
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HSSP; Q45894; IEIH.
SMR; P30995; 1-411.
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MEDLINE=90235864; PubMed=2185020;
Thompson D.E., Brehm J.K.; Oultram J.D., Swinfield T.-J., Shone C.C.,
Atkinson T., Melling J., Minton N.P.;
"The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding
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MEDLINE=97016817; PubMed=8863443;
MEDLINE=97016817; PubMed=8863443;
Bast A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
"Organization and phylogenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component.";
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Binz T., Kurazono H., Wille M., Frevert J.; Wernars K., Niemann H.;
"The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.";
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                                              01-JUL-1989 (Rel. 11, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
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12-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last sequence)
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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int. J. Syst. Bacteriol. 46:1105-1112(1996).
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Biochem. Biophys. Res. Commun. 162:1388-1395(1989).
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                                                                                                                                                                                                                                                                                                                                                                          chain; Botulinum neurotoxin A heavy-chain]
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MEDLINE-98455071; PubMed-9783750;
Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
"Crystal structure of botulinum neurotoxin type A and implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Furict. Biol. 5:898-902(1998).
FUNCTION: Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-din-[-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain (H).
-!-.SUBCELLULAR LOCATION: Secreted.
-!- PHARMACEUTICAL: Available under the name BOTOX (Allergan) for the
treatment of strabismus and blepharospasm associated with dystonia
                                                                                                                                                                                                      PROTEIN SEQUENCE OF 448-482.

MEDLINE=85285016; PubMed=3896784;
Shone C.C., Hambleton P., Melling J.;
Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
COFACTOR: Binds 1 zinc ion per subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94124495; PubMed-8224407;
Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
Jahn R., Niemann H.,
Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
J. Biol. Chem. 269:1617-1620(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and 18 kD fragments."; J. Protein Chem. 12:351-363(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: Binds 1 zinc ion per subunit. SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94063091; PubMed-8243676; DOI=10.1016/0014-5793(93)80448-4; Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J., Benfenati F., Wilson M.C., Montecucco C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds."; FRBS Lett. 335:99-103(1993).
                                                                                                R.L.;
eavy chain into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
MEDLINE=21556941; PubMed=11700044; DOI=10.1006/bbrc.2001.5911;
Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
"Site-directed mutagenesis identifies active-site residues of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Limited hydrolysis of proteins of
                                                                                                    Niece R.L.,
the heavy o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ight chain of botulinum neurotoxin type a."
                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 866-879 AND 1147-1218.
                                                                                                    Sathymoorthy V., Dasgupta B.R., Foley J., "Botulinum neurotoxin type A: cleavage of
                                                                                                                                             halves and their partial sequences.";
Arch. Biochem. Biophys. 266:142-151(1988)
                                                             AND 872-895
and around the nicking site.";
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                                                                                  MEDLINE=89024662; PubMed=3178218;
                                                                                                                                                                                                                                                                                                                                  J. Biochem. 151:75-82(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                   Gimenez J.A., DasGupta B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION OF SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION OF SUBSTRATE
                                                               PROTEIN SEQUENCE OF 448-474
                     Biochimie 72:661-664 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8397793;
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                                                                                                                                                                                                                                    This Swise-Prot entry is copyright. It is produced through a collaboration between the Swise Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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and cervical dystonia. Also used for the treatment of hemifacial spasm and a number of other neurological disorders characterized by abnormal muscle contraction.

In SURLANESOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, B, F, and G.

I SIMILARITY: Belongs to the peptidase M27 family.

I DATABASE: NAME-BOTOX product information Web site;
WWW-http://www.botox.com/site/".

I DATABASE: NAME-Protein Spotlight; NOTE-Issue 19 of February 2002;
WWW-"http://www.expass.org/spotlight/back_issues/spit[0].shifm]".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR011591; Botulinum.

R InterPro; IPR011591; Botulinum.

R InterPro; IPR0106055; Pept M Zn BS.

R InterPro; IPR0103928; Toxin_treng M27.

R InterPro; IPR012500; Toxin_trens.

R Pfan; PF01952; Toxin_trans.

R Pfan; PF07952; Toxin_trans; 1.

R PRINTS; PR007056; BORNTOXILYSIN.

R PRINTS; PR007056; BORULinum; 1.

R PROSITE; PS00142; ZINC_PR0TEASE; 1.

R 3D-gructure; Direct procein sequencing; Hydrolase; Metal-binding; Metalloprotease; Direct process; Pharmaceutical; Protease; Toxin; Transmembrane; Zinc.
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; Pred. No. 4.1e-18;
21; Mismatches 50; Indels 13; Gaps
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Zinc (catalytic).
Zinc (catalytic).
Zinc (catalytic).
Interchain (between light and heavy
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E->A: Drastic decrease in enzymatic
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Botulinum neurotoxin A heavy-chain.
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EMBL; M30196; AAA23262.1; -; Genomic_DNA.

EMBL; X5973; CAA63551.1; -; Genomic_DNA.

EMBL; D67030; BAA11051.1; -; Genomic_DNA.

EMBL; M27892; AAA23269.1; -; Genomic_DNA.

PDB, 35294; BTCLAB.
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RESULT 12 Q7B8V4\_CLOBO

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KIIKLIRTSNSNNSLGQIIVMDS-----IGNNCTWNFQNNNGGNIGLLGFHSNN----LV 111
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MEDLINE=22919384; Pubmed=14557061; DOI=10.1016/80378-1119(03)00792-3;
MEDLINE=22919384; Pubmed=14557061; DOI=10.1016/80378-1119(03)00792-3;
Zhang L., Lin W.J., Li S., Aoki K.R.;
"Complete DNA sequences of the botulinum neurotoxin complex of
Clostridium botulinum type A-Hall (Allergan) strain.";
Gene 315:21-32(2003)
EMBL; AF461540; AAM75961.1; -; Genomic_DNA.
EMBL; AF488749; AAQ06331.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Gaps
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STRAIN-TYPE A / Kyoto-F;
MEDLINE-94143603; PubMed-8310180; DOI=10.1016/0923-2508(93)90004-L;
MEDLINE-94143603; PubMed-8310180; DOI=10.1016/0923-2508(93)90004-L;
Willems A., East A.K., Lawson P.A., Collins M.D.;
"Sequence of the gene coding for the neurotoxin of Clostridium
botulinum type A associated with infant botulism: comparison with
other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
                                                                                                                                                                                                                                       STRAIN-Hall A-hyper;
MEDLINE-22617869; PubMed=12732962; DOI=10.1007/s00284-002-3851-1;
Dineen S.S., Bradshaw M., Johnson E.A.;
"Neurotoxin gene clueters in Clostridium botulinum type A strains: sequence comparison and evolutionary implications.";
Curr. Microbiol. 46:345-352(2003).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
(Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain].
                                                                                                       Clostridium botulinum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=botA; Synonyms=atx, bna;
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1296;
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                           Last sequence update)
Last annotation update)
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      Created)
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                                                                BONT/A (Neurotoxin BONT).
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hes 67; Conserv
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                                              10-MAY-2005
                                                                                       Name=bont/a;
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BXA2_CLOBO
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Matches
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East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

T. "Organization and phylosenetic interrelationships of genes encoding components of the botulinum toxin complex in proteolytic Clostridium toxin complex in proteolytic Clostridium toxin complex in proteolytic Clostridium toxin complex in proteolytic Clostridium toxin complex in proteolytic Clostridium toxin botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontroxic nonhemagglutinin component.";

Int. J. Syst. Bacteriol. 46:1105-112(1996).

Int. J. Syst. Daterriol. 46:1105-112(1996).

Int. J. Syst. Daterriol. 46:1105-112(1996).

The C-terminum toxin to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminum of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-[-Ag-198 bond in SNRP-25, thereby blocking results in Haccid paralysis, with frequent heart or respiratory failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H) (By similarity)

SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease; Toxin; Transmembrane; Linc.

INIT_MET 1 447 Botulinum neurotoxin A light-chain.

I GHAIN 448 1295 Botulinum neurotoxin A heavy-chain.

I TRANSMEM 626 646 Potential.

I TRANSMEM 655 675 Potential.

I ACT SITE 223 223 By similarity.

I METAL 226 226 Zinc (catalytic) (By similarity).

I METAL 226 226 Zinc (catalytic) (By similarity).

I DISULFID 1234 1279 By similarity.

I DISULFID 1234 1279 By similarity.

Chains) (By similarity).

SEQUENCE 1295 AA; 149280 MW; 5DA04Al3D98D6372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-structure; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: There are seven antigenically distinct forms botulinum neurotoxin: Types A, B, Cl, D, E, F, and G. SIMILARITY: Belongs to the peptidase M27 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD001963; Botulinum; 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X73423; CAA51824.1; -; Genomic_DNA.
EMBL; X87974; CAA61234.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1E1H; X-ray; A/C=9-249, B/D=250-415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR006025; Pept M_Zn BS.
Interpro; IPR000395; Peptidase M27.
Interpro; IPR012928; Toxin_recpt bd_N.
Interpro; IPR012928; Toxin_reans.
Pfam; PP01742; Peptidase M27; 1.
Pfam; PP07953; Toxin_R bind, N; 1.
Pfam; PP07952; Toxin_R bind, N; 1.
                                                                   PubMed=8863443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR011591; Botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00760; BONTOXILYSIN
                        NUCLEOTIDE SEQUENCE OF 1-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    failure (By similarity)
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1204 KILSALBIPDVGN-LSQVVVMKSKDDQGIRNKCKMNLQDNNGNDIGFIGFHLYDNIAKLV 1262
111
                                                                                      KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIIKLIRTSNSNNSLGQIIVMDS-----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of Clostridium botulinum Strains Associated with Infant Botulism Case in the United Kingdom.", J. Clin. Microbiol. 0:0-0(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith T.J., Lou J., Geren I., Forsyth C., Tsai R., Tepp W.H., Bradshaw M., Johnson B.A., Smith L.A., Marks J.D.; Sequence variation within botulinum neurotoxin serotypes impacts antibody binding and neutralization."; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Johnson B.A., Tepp W.H., Bradshaw M., Gilbert R.J., Cook P.E.,
McIntosh E.D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1296 AA; 149410 MW; 6F12E7BF28ED69D1 CRC64;
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Last annotation update)
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43.4%; Pred. No. 2.1e-17;
tive 22; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type A2 botulinum neurotoxin.
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Clostridium botulinum.
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                                                                                                                                                                                                                                                                                                                                                                                                            OSBGH1_CLOBO PRELIMINARY;
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nes 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FRI-H1A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1491;
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Gaps

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Length 1295; Indels

39.4%; Score 298.5; DB 1; 43.4%; Pred. No. 2.1e-17;

ilarity 43.4%; Pred. No. 2.1e-Conservative 22; Mismatches

Query Match Best Local Similarity Matches 66; Conserv

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NUCLECTIDE SEQUENCE.

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24.8%; Score 188; DB 2; Length 77;
Best Local Similarity 97.4%; Pred. No. 4.2e-09;
Matches 37; Conservative 0; Mismatches 1; Indels
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Search completed: March 2, 2006, 00:46:26 Job time: 75.3248 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

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(without alignments) 672.325 Million cell updates/sec

US-08-981-087B-4 757 Title: Perfect score:

1 NIFSNTRLYTGVEVIIRKNG......TSSNGCFWSFISKEHGWQEN 143 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 seqs, 82675679 residues Searched:

572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

yued Patents AA:\*
/cgn2\_6/ptodata1/iaa/5\_COMB.pep:\*
/cgn2\_6/ptodata1/iaa/6\_COMB.pep:\*
/cgn2\_6/ptodata1/iaa/H\_COMB.pep:\*
/cgn2\_6/ptodata1/iaa/H\_COMB.pep:\*
/cgn2\_6/ptodata1/iiaa/RE\_COMB.pep:\*
/cgn2\_6/ptodata1/iiaa/RE\_COMB.pep:\*
/cgn2\_6/ptodata1/iiaa/RE\_COMB.pep:\* Issued Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Sequence 9, Appli	6	-	23,	23,	N	26,	Sequence 26, Appl	26,	26,	28,	28,	28,	28,	213	_	55	• •	Sequence 2, Appli	4,	œ	Sequence 2, Appli	Sequence 4, Appli	5,	17,	16,	Sequence 15, Appl
SUMMAKIES	ID	US-09-288-326A-9	US-09-548-409B-9	US-08-480-604A-23	US-08-405-496A-23	US-08-915-136-23	US-09-084-517-23	US-08-480-604A-26	US-08-405-496A-26	US-08-915-136-26	US-09-084-517-26	US-08-480-604A-28	US-08-405-496A-28	US-08-915-136-28	US-09-084-517-28	US-10-360-101-219	US-09-465-276-1	US-08-446-114A-22	US-10-360-101-220	US-07-618-312A-2	US-07-618-312A-4	US-08-110-786A-8	US-08-280-228-2	US-08-280-228-4	US-08-668-381A-5	US-08-913-880C-17	US-08-913-880C-16	US-08-913-880C-15
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	Score	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	306.5	298.5	281.5	277.5	149	137	137	137	137	137	137	137	137	137
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Sequence 14, Appl Sequence 13, Appl Sequence 12, Appl	4 ~ ~ 1	Sequence 24925, A Sequence 3, Appli Sequence 22484, A	Sequence 3, Appli Sequence 570, App	Sequence 569, App Sequence 19247, A	Sequence 2, Appli Sequence 2, Appli	Sequence 1, Appli Sequence 72, Appl	Sequence 71, Appl
US-08-913-880C-14 US-08-913-880C-13 US-08-913-880C-12	US-08-913-88UC-11 US-08-913-88UC-10 US-08-913-88UC-1	US-09-248-796A-24925 US-08-415-751-3 US-09-248-796A-22484	US-09-465-276-3 US-09-830-230A-570	US-09-830-230A-569 US-09-248-796A-19247	US-09-697-367-2 US-09-918-909A-2	US-08-375-100-1 US-09-418-710-72	US-09-839-479-71
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## ALIGNMENTS

1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60 Indels 13; Length 382; APPLICANT: Aoki, K. Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treatment of Pancreatitis
TITLE OF INVENTION: Treatment of Pancreatitis
FILE REPERBNCE: 17282
CURRENT APPLICATION NUMBER: US/09/288,326A
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 382 Query Match
40.5%; Score 306.5; DB 2;
Best Local Similarity 44.4%; Pred. No. 2.7e-25;
Matches 67; Conservative 21; Mismatches 50; Sequence 9, Application US/09288326A Patent No. 6776990 GENERAL INFORMATION: APPLICANT: Steward, Lance E. ; ORGANISM: Clostridium Botilinum US-09-288-326A-9 US-09-288-326A-9 61 TYPE: PRT ò 셤

Gaps

KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111 290 KILSALEIPDVGN-LSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLV 348 APPLICANT: Aoki, K. Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treament of Pancreatitis
FILE REPERENCE: 17282CIP(AP)
CURRENT APPLICATION NUMBER: US/09/548,409B 112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWOE 142 ||:|| | ::::|| | |:|| ASNWYNRQIERSSRTLGCSWEFIPVDDGWGE 379 Sequence 9, Application US/09548409B Patent No. 684399B GENERAL INFORMATION:
APPLICANT: Steward, Lance E. US-09-548-409B-9 349 ò ద ò 셤

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GENERAL INFORMATION

APPLICANT: KINK, JOHN A.

APPLICANT: THALLEY, BRUCE S.

APPLICANT: TATALEY, BRUCE S.

APPLICANT: TATALEY, BRUCE S.

APPLICANT: TATAFORD, DOUGLAS.

TITLE OF INVENTION: VACCINE AND ATTIOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE

NUMBER OF SEQUENCES 32

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN & CARROLL, LLP

STREET: 220 WONTOCHENES: SIZE

COMPATE: LANGENCE ADDRESS:

ADDRESSER: MEDLEN & CARROLL, LLP

STREET: 220 WONTOCHENES: SIZE

COMPATE: CALIFORNIA

COMPUTER: READABLE FORM:

MEDLUM TYPE: PACHOL STREE OF AMERICA

COMPUTER: LBM PC COMPATIBLE OOK

COMPUTER: LBM PC COMPATIBLE OOK

COMPUTER: LBM PC COMPATA: PEL-BOS OF ARELICATION NUMBER: US 08/422,711

FILING DATE: 14-APR-1995

PRICH APPLICATION NUMBER: US 08/405,496

PRICH APPLICATION NUMBER: US 08/405,496

PRICH APPLICATION NUMBER: US 08/161,907

PRICH APPLICATION NUMBER: US 08/161,907

PRICH APPLICATION NUMBER: US 08/161,907

PRICH APPLICATION NUMBER: US 08/161,907

PRICH APPLICATION NUMBER: US 08/161,907

PRICH APPLICATION NUMBER: US 07/985,321

PRICH APPLICATION NUMBER: US 08/161,907

PRILING DATE: 0-DEC-1992

PRICH APPLICATION NUMBER: US 08/161,907

PRILING APPLICATION NUMBER: US 08/161,907

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PRILING APPLICATION NUMBER: US 08/161,907

PRILING APPLICATION NUMBER: US 08/161,907
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40.5%; Score 306.5; DB 2; Length 382;
Best Local Similarity 44.4%; Pred. No. 2.7e-25;
Matches 67; Conservative 21; Mismatches 50; Indels 13;
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CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 09/288,326
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-480-604A-23
; Sequence 23, Application US/08480604A
; Patent No. 5736139
                                                                                                                                                                                                                                                                      ORGANISM: Clostridium botulinum
                                                                                                                                                                                                                                                                                                     US-09-548-409B-9
                                                                                                                                                                                                        LENGTH: 382
                                                                                                                                                                                                                                              TYPE: PRT
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289 NIYLNSSLYRGTKFIIKKYAS---GNKDNIVRNDRVYINVVVKNKEYRLATNASQAGVE 345
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Sequence 23, Application US/08405496A
Patent No. 5919665
Patent No. 5919665
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NUCLOTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: FLOPPY GIBE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 31-OCT-1999
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1999
ATTORNEY/AGENT INFORMATION:
NAME: INGOLLA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
40.5%; Score 306.5; DB 1;
Best Local Similarity 44.4%; Pred. No. 3.2e-25;
Matches 67; Conservative 21; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 ASNWYNRQIERSSRTLGCSWEFIPVDDGWGE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQE 142
                                                        NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REPERBNICH/COKKI NUMBER: 0PHD-01763
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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UMBER: US 08/329,154
25-OCT-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                                     TELEFAX: (15) 397-8310
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acida
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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04-DEC-1992
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amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-915-136-23
                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
  FILING DATE:
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                                                                                                                                                                                                                                                                                                         Gaps
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40.5%; Score 306.5; DB 1; Length 438;
Best Local Similarity 44.4%; Pred. No. 3.2e-25;
Matches 67; Conservative 21; Mismatches 50; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: MEDLEN & CARROLL, LLP
220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWOE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTITOXIN
REGISTRATION NUMBER: 40,027
REPERBNICH/DOCKET NUMBER: OPHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECTLE TYPE: protein
US-08-405-496A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
PILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/08915136
Patent No. 6290960
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-915-136-23
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289 NIYLNSSLYRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVE 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 13; Gaps
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APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS: URBY OF CREDIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 438;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
40.5%; Score 306.5; DB :
Best Local Similarity 44.4%; Pred. No. 3.2e-25.
Matches 67; Conservative 21; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTCOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 ASNWYNROIERSSRTLGCSWEFIPVDDGWGE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ASSWYYNNIRKNISSNGCFWSFISKEHGWOE 142
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REPERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/09084517
Patent No. 6613329
GENERAL INFORMATION:
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US-08-480-604A-26
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISTA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS:
ADDRESSEE: ABDLENE CARROLL, LLP STREET: 220 MONIGOMERY STREET, SUITE 2200
STARET: AN FRANCISCO STATES OF AMERICA
STAFF CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
40.5%; Score 306.5; DB 2; Length
Best Local Similarity 44.4%; Pred. No. 3.2e-25;
Matches 67; Conservative 21; Mismatches 50; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TaM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version.#1.30
SOFTWARE: Patentin Release #1.0, Version.#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-00N-1995
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
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FILING DATE: 31-CCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01610
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acide
TYPE: amino acide
                                                                                                                                                                      OPHD-01610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION:
04-DEC-1992
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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US-08-480-604A-26
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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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Query Match

40.5%; Score 306.5; DB 1; Length 462;
Best Local Similarity 44.4%; Pred. No. 3.5e-25;
Matches 67; Conservative 21; Mismatches 50; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A,
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SUQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: MEDIANES & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk Computible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A FILING DATE: 16-MAR-1995 CLASSIFICATION 1424 PRIOR APPLICATION DATA: APPLICATION DATE: US/08/329,154 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATE: US/08/161,907 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQE 142
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PRICING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DAYE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: UNGOLIA, DIAME E.
REGISTRATION NUMBER: 40,027
FILING DATE: 104-DEC-1989
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEG DI NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-405-496A-26
; Sequence 26, Application US/08405496A
; Patent No. 5919665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 462 amino acids
amino acid
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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Patent No. 6613329
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSE: ANDRESSE: ANDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
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ZIP: 94104

ZIP: 94104

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PROCOMPATER: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.5%; Score 306.5; DB 2; 44.4%; Pred. No. 3.5e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
40.5%; score sver, Lest Local Similarity 44.4%; Pred. No. 3.5e-Matches 67; Conservative 21; Mismatches
                                                         PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/965,321
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTONNEY, AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTATION NUMBER: 40,027
REPERENCY DOCKET NUMBER: 00PD-01763
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                        US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
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                        APPLICATION NUMBER: US 0 FILING DATE: 25-OCT-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // MOLECULE TYPE: protein US-08-915-136-26
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APPLICANT: THALLEY, BRUCE S.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE NUMBER OF ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, ILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
40.5%; Score 306.5; DB 1; Length 4
Best Local Similarity 44.4%; Pred. No. 3.5e-25;
Matches 67; Conservative 21; Mismatches 50; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWQE 142
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-05C-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.

REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acide
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear

MOLECTLE TYPE: protein
US-08-405-496A-26
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APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
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COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08915136
Patent No. 6290960
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CALIFORNIA
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| Patent No. 5736139
| GENERAL INFORMATION:
| APPLICANT: KINK, JOHN A. |
| APPLICANT: THALLEY, BRUCE S. |
| APPLICANT: THALLEY, DOGLAS. |
| APPLICANT: PADHYE, NISHA V. |
| APPLICANT: PADHYE, NISHA V. |
| APPLICANT: PADHYE, NISHA V. |
| APPLICANT: PADHYE, NISHA V. |
| APPLICANT: PADHYE, NISHA V. |
| APPLICANT: PADHYE, STAFFORD, DOUGLAS. C. |
| TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND |
| TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE |
| NUMBER OF SEQUENCES: |
| ADDRESSEE: MEDIEN & CARROLL, LLP |
| STREET: 220 MONTGOMERY STREET, SUITE 2200 |
| STATE: CALIFORNIA |
| COUNTRY: UNITED STATES OF AMERICA |
| COUNTRY: UNITED STATES OF AMERICA |
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44.4%; Pred. No. 3.5e-25;
tive 21; Mismatches 50;
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                                                                                                   PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/965,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/929,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REPERENCE/DOCKET NUMBER: OPHD-01610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 39-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.4%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-084-517-26
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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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; Patent No. 5919665
; GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
40.5%; Score 306.5; DB 1;
Best Local Similarity 44.4%; Pred. No. 1.4e-24;
Matches 67; Conservative 21; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1263 ASNWYNRQIERSSRTLGCSWEFIPVDDGWGE 1293
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                                                                     PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 13-OCT-1999
ATTORNEY/AGENT INFORMATION:
NAME: TANGOLIA DATA:
ANDELSON DATE: 31-OCT-1999
ATTORNEY/AGENT INFORMATION:
NAME: TANGOLIA DATAMED BY TANKED BY TA
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REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
                                            14-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-480-604A-28
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COMPUTER READABLE FORM:
APPLICATION NUMBER:
FILING DATE: 14-API
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1296 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STREET: 220 MONTGOMERY
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-915-136-28
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOC
                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
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Best Local Similarity
                                                                    FILING DATE:
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US-09-084-517-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, JOSEPH N.
APPLICANT: PIRCA, JOSEPH N.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.5%; Score 306.5; DB 1
Best Local Similarity 44.4%; Pred. No. 1.4e-24;
Matches 67; Conservative 21; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
CITY: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWQE 142
                                                                  PILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
PILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
PILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1998
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                           OPHD-01308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
                                                  APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-915-136-28
; Sequence 28, Application US/08915136
; Patent No. 6290960
                                                                                                                                                                                                                                                                                                       40,027
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: OP TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
                                                                                                                                                                                                                                                                                                                                                                 (415) 705-8410
16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    NAME: INGOLIA, DIANE
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.5%; Score 306.5; DB 2; Length 1296; 44.4%; Pred. No. 1.4e-24;
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Patent No. 6613329
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: WILLLAMS, JAMES A.
APPLICANT: WILLLAMS, JAMES A.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICLE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ASSWYYNNIRKNTSSNGCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                               FILING DATE: 16-WAR-1995
FILING DATE: 16-WAR-1995
RELORATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
FILING DATE: 25-OCT-1994
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
FRIUNG DATE: 31-OCT-1889
FILING DATE: 31-OCT-1889
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPHD-01763
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                                                                                                                US 08/405,496
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COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPH
TELECOMMUNICATION: TELECOMMUNICATION: (415) 705-8410
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Indels 13; Gaps

DB 2; Length 848;

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61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNPQNNNGGNIGLLGFHSNN----LV 111
                                                                                                                                                    1 NIFSWITELYTGVEVIIRKNGSTDISNITDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                     Query Match 39.4%; Score 298.5; DB 2; Best Local Similarity 43.4%; Pred. No. 5.9e-24; Matches 66; Conservative 22; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                    112 ASSWYYNNIRKNISSNGCFWSFISKEHGWQEN 143
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Job time : 17.5847 secs
         US-10-360-101-219
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Patent No. 686126
GENERAL INFORMATION:
PAPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantiblotic way
TITLE REFERENCE: 2183-6573
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.1
SEQ ID NO 219
LENGTH: 848
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VEGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: sequence A-heavy chain of clostridium botulinum toxin type A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1147 NIYLNSSLYRGTKFIIKKYAS---GNKDNIVRNNDRVYLNVVVKNKEYRLATNASQAGVE 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 40.5%; Score 306.5; DB 2; Length 1296; l Similarity 44.4%; Pred. No. 1.4e-24; 67; Conservative 21; Mismatches 50; Indels 13; Gaps
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,517
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                                                                                   FILLING JATE:

CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1993
PRIOR APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT: NEORMATION:
NAME: CARROLL, PETER G.
RECERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 0PHD-01610
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 795-8410
TELEPAN: (415) 397-8338
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 and no ocide
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TOPOLOGY: linear
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US-10-360-101-219
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Best Local S:
Matches 67
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// MOLECULE TYPE: peptide US-08-981-087A-4
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                                                                                                March 2, 2006, 01:11:03; Search time 56.9014 Seconds (without alignments) 1050.055 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                       1 NIFSNTRLYTGVEVIIRKNG.....TSSNGCFWSFISKEHGWQEN 143
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA_Main:*
... /cgnz 6/prodate/1/pubpaA/US07 PUBCOMB.pep:*
... /cgnz 6/prodata/1/pubpaA/US08 PUBCOMB.pep:*
... /cgnz 6/prodata/1/pubpaA/US10A PUBCOMB.pep:*
... /cgnz 6/prodata/1/pubpaA/US10A PUBCOMB.pep:*
... /cgnz 6/prodata/1/pubpaA/US10B PUBCOMB.pep:*
... /cgnz 6/prodata/1/pubpaA/US10B PUBCOMB.pep:*
... /cgnz 6/prodata/1/pubpaa/US10B PUBCOMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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192
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Perfect score:
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Sequence	Sequence	Sequence	Seguence						Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Sequence.	Sequence
US-10-728-696-73	US-11-001-241-73	US-10-354-774-71	US-10-271-012-71	US-10-452-024-6	US-10-729-122-71	US-10-729-039-71	US-10-729-527-71	US-10-727-898-71	US-10-728-696-71	US-11-001-241-71	US-10-452-024-156	US-10-452-024-127	US-09-910-186A-14	US-10-354-774-56	US-10-271-012-56	US-10-729-122-56	US-10-729-039-56
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448	448	1274	1274	1274	1274	1274	1274	1274	1274	1274	1268	1251	449	452	452	452	452
80.2	80.2	80.2	80.2	80.2	80.2	80.2	80.2	80.2	80.2	80.2	9.94	55.2	53.0	53.0	53.0	53.0	53.0
607	607	607	607	607	607	607	607	607	607	607	581	417.5	401	401	401	401	401
28	29	30	31	35	33	34	35	36	37	38	39	4 0	41	4.2	43	4	45
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## ALIGNMENTS

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APPLICANT: Ellore, Michael J.
APPLICANT: Mauchline, Margaret L.
APPLICANT: Manch, Nigel P.
APPLICANT: Pasechnik, Vladimir A.
APPLICANT: Titball, Richard W.
TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF CORRESPONDENCES. 6
CORRESPONDENCES. 6
                                                                                                                                                                                                                                                                                     8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,087A FILING DATE: 27-MAY-1998 CLASSIPICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          E: NIXON & VANDERHYE P.C.
1100 No. US20020081304Alth Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-70n-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9511909.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 9511909.5
FILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
Sequence 4, Application US/08981087A Publication No. US20020081304A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25,327
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                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 143 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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Query Match
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                                                                                            1 NIFSNIRLYTGVEVIIRKNGSIDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                          1 NIFSNITELYTGVEVIIRKNGSTDISNIDNFVRKNDLAXINVVDRDVEYRLYADISIAKPE
                                                        Gaps
                                                     .
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| Publication No. US20020081304A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Blmore, Michael J.
| APPLICANT: Minton, Migel P.
| APPLICANT: Titball, Richard W.
| APPLICANT: Titball, Richard W.
| TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF |
| NUMBER OF SEQUENCES. 6
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: NIXON & VANDERHYE P.C.
| STREET: 1100 No. US20020081304Alth Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Query Match
100.0%; Score 757; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 7.8e-68;
Matches 143; Conservative 0; Mismatches 0; Indels
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100.0%; Score 757; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 143; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,087A
FILING DATE: 27-MAY-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01409
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9511909.5
FILING DATE: 12-JUN-1995
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDULW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                 121 RKNTSSNGCFWSFISKEHGWQEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 431 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-08-981-087A-1
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289 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPF 348
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                                                                                 61 KIIKLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI
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Publication No. US2003000925A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
TITLE OF INVENTION: NEUROTOXIN
TITLE OF INVENTION: NEUROTOXIN
TITLE OF INVENTION: NEUROTOXIN
FILE REFERENCE: A33626-A 067252.0107
CURRENT FILING DATE: 2001-07-20
PRIOR PELICATION NUMBER: US/09/910,186A
PRIOR PELICATION NUMBER: 09/611,419
PRIOR PELICATION NUMBER: 60/133,865
PRIOR PELING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/133,865
PRIOR PELING DATE: 1999-05-12
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100.0%; Pred. No. 3.1e-67;
cive 0; Mismatches 0;
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Sequence 34, Application US/09910186A; Publication No. US20030009025A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 143; Conservative
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APPLICANT: Sutton, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REPREBENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: PCT/GB00/04644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562
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Pred. No. 5.2e-67;
100.0%; Pred. No. 3.1e-67; tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/GB02/02384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: synthetic construct US-10-130-973A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 008658.7
PRIOR FILING DATE: 2000-04-07
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Best Local Similarity 100.0%;
Matches 143; Conservative 0;
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SOFTWARE: PatentIn version 3.0
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  Best Local Similarity 100.
Matches 143; Conservative
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APPLICANT: Park, Jung-Beak
APPLICANT: Maksymowych, Andrew
ATLIA. OF INTERPREDIATION: Compositions and Methods For Transepithelial Molecular Transport
PILE REFERENCE: 9855-96U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRRNDLAYINVVDRDVEYRLYADISIAKPE 349
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         OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
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Pred. No. 3.1e-67;
                             TITLE OF INVENTION: NEUKOLOLING PILE REPERENCE: A35626-A 067222.0107
PILE REPERENCE: A35626-A 067222.0107
CURRENT APPLICATION NUMBER: US/09/910,186A
CURRENT FILING DATE: 2001-07-20
PRIOR PILING DATE: 2000-05-12
PRIOR PRILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-07-06
PRIOR PILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: 60/133,865
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SOFTWARE: FastSEQ for Windows Version 4.0
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R APPLICATION NUMBER: 60/133,866
R FILING DATE: 1999-05-12
R PILING DATE: 1999-05-12
R PILING DATE: 1999-05-12
R APPLICATION NUMBER: 60/133,868
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PRIOR APPLICATION NUMBER: 60/384,949
PRIOR FILING DATE: 2002-05-31
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Publication No. US20040013687A1
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-05-12
APPLICATION WUMBER: 60/133,869
ELING DATE: 1999-05-12
APPLICATION NUMBER: 60/133,873
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FILING DATE: 1993-09-21
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100.0%;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 178
LENGTH: 43.2
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Best Local Similarity 100.
Matches 143; Conservative
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US-10-130-973A-7
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US-10-478-516-6
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Sequence 6, Application US/10478516

Publication No. US20040208889A1

GENERAL INFORMATION:
APPLICANT: Sutton, John M.

APPLICANT: Shone, Clifford C.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FFLE REPERENCE: 1581.1000000

CURRENT APPLICATION NUMBER: US/10/478,516

FRICE RAPLICATION NUMBER: PTT/GB02/02384

PRIOR APPLICATION NUMBER: GB 0112687.9

PRIOR PLING DATE: 2002-05-21

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEC ID NOS: 32

SOFTWARE: Patentin version 3.1

SEQ ID NO S: 32

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/ OTHER INFORMATION: diphtheria toxin translocation domain with BONT/F-HC US-10-478-516-5
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Query Match
Best Local Similarity 100.0%; Pred. No. 5.2e-67;
Matches 143; Conservative 0; Mismatches 0; Indels
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100.0%; Score 757; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 143; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: GB 011
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 645
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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RESULT

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Sequence 7, Application US/10130973A
| Publication No. US20030147895A1
| Publication No. US20030147895A1
| GENERAL INFORMATION:
| APPLICANT: Stuton, John
| APPLICANT: Stuton, John
| TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
| TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
| FILE REFERENCE: 1581.092000
| CURRENT PAPLICATION NUMBER: US/10/10.30,973A
| CURRENT FILING DATE: 2002-10-21
| PRIOR APPLICATION NUMBER: GB 9928530.6
| PRIOR PELING DATE: 1999-12-02
| PRIOR FILING DATE: 1999-12-02
| PRIOR FILING DATE: 2000-04-07
| NUMBER OF SEQ ID NOS: 18
| SEGFWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: factor Xa linker, diphtheria toxin translocation domain, BoNT/F-F
US-10-478-516-7
Sequence 7, Application US/10478516;
Publication No. US2004020889A1
GENERAL INFORMATION:
APPLICANT: Sutton, John M.
APPLICANT: Shone, Clifford C.
TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins
FILE REPERENCE: 1581.1000000
CURRENT APPLICATION NUMBER: US/10/478,516
CURRENT APPLICATION NUMBER: US/2047802/02384
PRIOR APPLICATION NUMBER: GB 0112687.9
PRIOR PLING DATE: 2001-05-21
PRIOR PLING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Version 3.1
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100.0%; Score 757; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.6e-67;
Matches 143; Conservative 0; Mismatches 0;
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ORGANISM: Artificial sequence
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Sequence 26, Application US/10478516

Sequence 26, Application US/10478516

Publication No. US20040208889A1

GENERAL INFORMATION:

APPLICANT: SULton, John M.

APPLICANT: SULton, John M.

TITLE OF INVENTION: Pharmaceutical Use of Secreted Bacterial Effector Proteins

TILE REFERENCE: 1581.100000

CURRENT PILLNG DATE: 2003-11-24

PRIOR APPLICATION NUMBER: PCT/GB02/02384

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTHE: 979
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Pred. No. 7.7e-67;
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100.0%; Pred. No. 8.7e-67;
ive 0; Mismatches 0;
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 0086;
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 18
SCOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 887
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Best Local Similarity 100.0%;
Matches 143; Conservative 0
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ORGANISM: Artificial sequence
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Best Local Similarity 100.0
Matches 143; Conservative
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APPLICANT: Shone, Clifford
APPLICANT: Sutcon, John
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
FILE REFERENCE: 1581.0320000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: EPG9800/04644
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: GB 9928530.6
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-07
SPRIOR FILING DATE: 2000-04-07
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 862
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Sequence 6. Application US/10130973A
Publication No. US20030147895A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shone, John
APPLICANT: Silman, Nigel
TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells FILE REFERENCE: 1581.0920000
CURRENT APPLICATION NUMBER: US/10/130,973A
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: GB 9928530.6
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                               KIIKLIRISNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
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Best Local Similarity 100.0
Matches 143; Conservative
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US-10-130-973A-6
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Search completed: March
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       Sequence 15, Application US/10130973A

Publication No. US20030147895A1

Publication No. US20030147895A1

GENERAL INFORMATION:

APPLICANT: Shone, Clifford

APPLICANT: Stlman, Nigel

TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells

FILE REFERENCE: 1581.092000

CURRENT APPLICATION NUMBER: US/10/130,973A

CURRENT APPLICATION NUMBER: PCT/GB00/04644

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR FILING DATE: 190-04-07

NUMBER: PAGE 10 NOS: 18

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0
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Publication No. US20030147895A1

General INFORMATION:

APPLICANT: Shone, Clifford

APPLICANT: Sutton, John

APPLICANT: Slutton, John

APPLICANT: Slutton, John

APPLICANT: Slutton, John

TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells

FILE REFERENCE: 1581.092000

CURRENT FILING DATE: 2002-10-21

PRIOR FILING DATE: 2002-10-21

PRIOR PLICATION NUMBER: GP 2000-04644

PRIOR PPLICATION NUMBER: GB 928530.6

PRIOR PLING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0

SEQ ID NO 14

LENGTH: 1092
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Best Local Similarity 100.0%; Pred. No. 9.3e-67;
Matches 143; Conservative 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.0%; Pred. No. 1e-66;
Matches 143; Conservative 0; Mismatches 0; Indels 0;
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US-10-130-973A-15
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US-10-130-973A-14
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1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
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1 NIFSNTRLYTGVEVIIRKNG......TSSNGCFWSFISKEHGWQEN 143
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1: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
5: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
6: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
8: /cgn2 6/ptodata/1/pubpaa/US11 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                             Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

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	Description	Sequence 5, Appli	Sequence 8, Appli	Sequence 28, Appl	Sequence 26, Appl	Sequence 18, Appl	Sequence 3, Appli	Sequence 6, Appli	Sequence 20, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 30, Appl	Sequence 141, App	Sequence 24, Appl	Sequence 10263, A	Sequence 171, App	Sequence 22, Appl	Sequence 4021, Ap	Sequence 6679, Ap	Sequence 30, Appl	Sequence 1, Appli	Sequence 1312, Ap	Sequence 8445, Ap	Sequence 8731, Ap	Sequence 33, Appl	Sequence 95, Appl
SUMMARIES	ID	US/11/062	US/11/062	US-10-909-769-28	US-10-909-769-26	US-10-909-769-18	US/11/062	US/11/062	US-10-909-769-20	US/11/062	US/11/062	US-10-909-769-30	US-11-077-550-141	US-10-909-769-24	US-11-087-099-10263	US-11-052-554A-171	US-11-131-479-22	US-11-087-099-4021	US-11-087-099-6679	US-11-089-551A-30	US-11-052-554A-1	US-11-033-039-1312	US-11-087-099-8445	US-11-087-099-8731	US-11-089-551A-33	US-11-052-554A-95
	DB	-	7	9	9	9	7	7	9	7	7	9	7	9	7	۲	7	1	7	7	7	7	7	7	7	7
	Query Match Length DB	1059	1084	838	829	849	1067	1092	900	1070	1095	855	1315	834	874	2340	260	338	348	964	1268	260	244	701	710	1237
æ	Query Match	100.0	100.0	80.2	53.0	40.5	40.5	40.5	21.1	19.7	19.7	18.8	18.1	13.7	11.7	11.4	11.2	10.9	10.9	10.6	10.6	10.4	10.2	10.0	10.0	10.0
	Score	757	757	607	401	306.5	306.5	306.5	160	149	. 149	142.5	137	103.5	88.5	98	82	82.5	82.5	80	80	79	77	92	9/	9/
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RESULT 2 US/11/062

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Sequence 12160, A Sequence 22, Appl Sequence 92, Appl	Sequence 8, Appli Sequence 13, Appli Sequence 1, Appli Sequence 8, Appli	Sequence 34, Appl Sequence 339, App Sequence 19, Appl	7818, 6053, 358, 2	Sequence 358, App Sequence 3810, Ap Sequence 6480, Ap Sequence 6752, Ap Sequence 3774, Ap Sequence 134, App
US-11-087-099-12160 US-10-909-769-22 US-11-052-554A-92	US-10-510-947-8 US-11-042-988-13 US-11-135-235-1 US-10-873-528-8	US-11-089-551A-34 US-11-052-554A-339 US-11-133-360-19	US-11-133-346-19 US-11-087-099-7818 US-11-087-099-6053 US-10-131-826A-358	US-10-973-115B-358 US-11-072-512-3810 US-11-087-099-6480 US-11-087-099-3774 US-11-087-099-3774
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# ALIGNMENTS

US/11/062 RESULT 1

US/11/062 ; Sequence ; Publicati	/ll/062, Sequence 5, Application US/11062471A Publication No. US20050255093A1
GENERAL INF HAPPLICANT:	GENERAL INFORMATION: APPLICANT: SHONE, Clifford Charles ADD:17ANT: STITTON JOHN MARK
APPLICANT:	HALLIS,
, TITLE OF	HITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REF	FILE REFERENCE: 1581.0800001. CHRRRNT APPLICATION NUMBER: US/11/062,471A
CURRENT	FILING DATE: 2005-02-22
; PRIOR A	APPLICATION NUMBER: 09/831,050 PTLING DATE: 1999-11-05
	APPLICATION NUMBER: PCT/GB99/03699
	1-0
; PRIOR A	APPLICATION NUMBER: GB 9824282.9
NUMBER OF	F SEO ID NOS: 11
SOFTWARE	3: PatentIn Ver. 2.1
SEO ID NO	ß
; LENGTH: 1059	1059
; TYPE: PRT	
ORGANI	ORGANISM: Artificial Sequence
; FEATURE:	regiuns: OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a
US/11/062,471A-5	171A-5
Query Match	
Best Local Matches 14	Similarity 100.0%; Freu. NO. 13; Conservative 0; Mismatch
λ̈	1 NIFSNTRLYTGYEVIIRKNGSTDISNTDNEVRKNDLAYINVUDRDVEYRLYADISIAKPE 60
Dp	
λ٥	61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYNNNI 120
qq	977 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 1036
δά	121 RKNTSSNGCFWSFISKEHGWQEN 143
Db 1	1037 RKNTSSNGCFWSFISKEHGWQEN 1059

linker,

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Sequence 18, Application US/10909769

Publication No. US20060024331A1

GENERAL INFORMATION:

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Steward, Lance E.

APPLICANT: Sachs, George

TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteria;

TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteria;

TITLE OF INVENTION: 100 (ROI2003-146)

CURRENT APPLICATION NUMBER: US/10/909,769

CURRENT FILING DATE: 2004-08-02

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.3

SEQ ID NO 18

LENGTH: 849

TYPE: PRT

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Andi, Kei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteris
FILE REFERENCE: ALLEGO10-100 (RO12003-146)
CURRENT APPLICANTON NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 26
LENGTH: 829
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     61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNPQNNNGGNIGLLGFHSNNLVASSWYNNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 KLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNIRKN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.0%; Score 401; DB 6; Length 829; Best Local Similarity 55.4%; Pred. No. 2e-32; Matches 77; Conservative 26; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-26
                                                                                                                                                                                                   121 RKNTSSNGCFWSFISKEHGWQE 142
                                                                                                                                                                                                                                             817 RRNTSSNGCFWSSISKENGWKE 838
                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-10-909-769-18
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wel-Jen
APPLICANT: Lin, Wel-Jen
APPLICANT: Aoki, Kel Roger
APPLICANT: Aoki, Kel Roger
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characterist
FILE REFERENCE: ALL: Toxin Compounds with Enhanced Membrane Translocation Characterist
CURRENT APPLICATION NUMBER: US/10/909,769
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   942 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KIIKLIRTSNSNNSLGQIIVMDSIGNNCTMNFQNNNGGNIGLLGFHSNNLVASSWYYNNI 120
                                                                           APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Charles
APPLICANT: SHONE, Clifford Mark
APPLICANT: SUTTON, John Mark
APPLICANT: SILMAN, Nigel
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPRENDE: 1891.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT APPLICATION NUMBER: US/21/050
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR PILING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 8
LENGTH: 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 757; DB 7; Length 1084; Best Local Similarity 100.0%; Pred. No. 5.8e-68; Matches 143; Conservative 0; Mismatches n. 7-3-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 838;
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80.2%; Score 607; DB 6;
Best Local Similarity 83.1%; Pred. No. 4.6e-53;
Matches 118; Conservative 8; Mismatches 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1062 RKNTSSNGCFWSFISKEHGWQEN 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 RKNTSSNGCFWSFISKEHGWQEN 143
Sequence 8, Application US/11062471A Publication No. US20050255093A1 GENERAL INFORMATION:
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Publication No. US20060024331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60

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; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M
US/11/062,471A-6
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APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Lin, Wei-Jen
APPLICANT: Acki, Kei Roger
APPLICANT: Sachs, George
APPLICANT: Acki, Kei Roger
APPLICANT: Acki, Kei Roger
APPLICANT: Sachs, George
APPLICANT: ALENOUB-100 (ROIZ003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT PAPLICATION NUMBER: US/10/909,769
CURRENT PAPLICATION NOS: 34
SOFTWARE: PATENTIN PAPEL S.004-08-02
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 20
LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KIIKLIRTSNSNNSLGQIIVMDS----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NIFSNIRLYTGVEVIIRKNGSTDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
                                         APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KIIKLIRTSNSNNSLGQIIVM---DSIGNNCTMNFQNN--NGGNIGLLGFH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1092;
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21.1%; Score 160; DB 6; Length 900;
Best Local Similarity 29.2%; Pred. No. 3.1e-08;
Matches 47; Conservative 28; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.5%; Score 306.5; DB 7;
44.4%; Pred. No. 8.2e-23;
vative 21; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1059 ASNWYNRQIERSSRTLGCSWEFIPVDDGWGE 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 ASSWYYNNIRKNISSNGCFWSFISKEHGWOE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-20
                                                                             FILE REPERENCE: 1581.080001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 2005-02-22
RELOR APPLICATION NUMBER: 09/831,050
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6 **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 20, Application US/10909769; Publication No. US20060024331A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
SUTTON, John Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                         KIIKLIRTSNSNNSLGQIIVMDS-----IGNNCTMNFQNNNGGNIGLLGFHSNN----LV 111
                                                                                                                                                                                                                                                                                              APPLICANT: STUTION, JOHN Mark
APPLICANT: STUMM, Mark
APPLICANT: STUMM, Nigel
APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
TITLE OF INVENTION DELivery of Superoxide Dismutase to Neuronal
CURRENT FILING DATE: 1080001
CURRENT FILING DATE: 1090-11-05
PRIOR PELICATION NUMBER: 09/831,050
PRIOR PELICATION NUMBER: PCT/GB99/03699
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: GB 9824282.9
PRIOR PELING DATE: 1999-11-05
PRIOR PELING DATE: 1999-11-05
SOFTWARE: PALENTIN NUMBER: GB 9824282.9
PRIOR PELING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 3
LENGTH: 1067
                                                                                                                                                                              1 NIFSNITRLYTGVEVIIRKNGSIDISNIDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPE
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                                                                                                                                       Gaps
                                                                                                                                       13;
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                                                                                         Length 849;
                                                                                           Score 306.5; DB 6; Length 8
Pred. No. 6.1e-23;
21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 40.5%; Score 306.5; DB 7; Best Local Similarity 44.4%; Pred. No. 8e-23; Matches 67; Conservative 21; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1034 ASNWYNROIERSSRTLGCSWEFIPVDDGWGE 1064
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                                                                                                                                                                                                                                                                                                                                                            112 ASSWYYNNIRKNISSNGCFWSFISKEHGWOE 142
                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Amino acid sequence of HC US-10-909-769-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/11062471A Publication No. US20050255093A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/11062471A Publication No. US20050255093A1
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APPLICANT: SHONE, Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clifford Charles
                                                                                                                                       21;
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ORGANISM: Artificial Sequence
                                                                                           40.5%;
ilarity 44.4%;
Conservative 2
                                                                                                                Similarity
                                                                                                                                    67;
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                                                                                             Query Match
Best Local S
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      FEATURE:
                                                                                                                                         Matches
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Gaps

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NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2
SEQ ID NO 7
LENGTH: 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 EKLFLSIISDSNEFYKTIEIKEYDEQPSYSCQLLFKKDERSTDDIGLIGIHRFYESGVLR 859
                                                                                                                                                                                                          Sequence 4, Application US/11062471A
| Sequence 4, Application US/11062471A
| Publication No. US20050255093A1
| GENERAL INFORMATION:
| APPLICANT: SHONE. Clifford Charles
| APPLICANT: SUTTON, John Mark
| APPLICANT: SUTTON, John Mark
| APPLICANT: SILMAN: Nigel
| TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
| FILE REFERENCE: 1581.0800001
| CURRENT APPLICATION NUMBER: US/11/062,471A
| CURRENT PELLING DATE: 1999-11-05
| PRIOR FILING DATE: 1999-11-05
| PRIOR PILING DATE: 1999-11-05
| PRIOR PILING DATE: 1999-11-05
| PRIOR PILING DATE: 1999-11-05
| PRIOR PILING DATE: 1999-11-05
| PRIOR FILING DATE: 1999-11-05
| RINDER OF SEQ ID NOS: 11
| SOFTWARE: Patentin Ver. 2.1
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APPLICANT: SUTTON, John Mark
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: HALLIS, Bassam
APPLICANT: SILMAN, NIGE1
ITILE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REPERENCE: 1581.0800001
CURRENT APPLICATION NUMBER: US/11/062,471A
CURRENT FILING DATE: 1005-02-22
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
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19.7%; Score 149; DB 7; Length 1070;
Best Local Similarity 26.6%; Pred. No. 4.8e-07;
Matches 41; Conservative 28; Mismatches 65; Indels 2
                                                                    107 --- SNNLVASSWYYNNI-RKNTSSN-GCFWSFISKEHGWQE 142
                                                                                                  860 KKYKDYPCISKWYLKEVKRPYKSNLGCNWQFIPKDEGWTE 900
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ORGANISM: Artificial Sequence
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Steward, Lance E.
APPLICANT: Abi, Wal-Jen
APPLICANT: Abi, Wel-Jen
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteris
FILE REFERENCE: ALLE0010-100 (ROI2003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NO 3.0
LENGTH: 855
                                                                                 OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human
                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                             19.7%; Score 149; DB 7; Length 1095; 26.6%; Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----HSNNLVASSWYYNNIRKNTSS--NGCFWSFISKEHGWQE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 VASSWYYNNIRKN--TSSNGCFWSFISKEHGWOE 142
                                                                                                                                                                                                                 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Amino acid sequence of HC
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; Sequence 141, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
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. Sequence 30, Application US/10909769

. Publication No. USZ0060024331A1

. GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 41, Conservative
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Sequence 171, Application US/11052554A
Publication No. US2005028866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT APPLICATION AND ADDITIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
CURRENT APPLICATION NUMBER: US/11/052,554A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KIIKLIRTSNSNNSLGQIIVMDSIGN--NCTMNFQNNNG-GNIGLLGFHSNNLVASSWYY 117
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                                                                                                                                                                                                                                                                                                                                                                                                      ----SNGCFWSFISKEHG 139
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                                                                                                                               6 TRLYTGVEVIIR----KNGSTDISNTDNFVRK---NDLAYINVVDRDVEYRLYADISIAK 58
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                                                                                                                                                                         Gaps
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                                                                 79;
Length 834;
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                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 10263
13.7%; Score 103.5; DB 6; llarity 21.9%; Pred. No. 0.013; Conservative 22; Mismatches 42;
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28.5%; Pred. No. vo.
22; Mismatches
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PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10263, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Clostridium acetobutylicum
US-11-087-099-10263
                                                                                                                                                                                                                                                                                                                                                                                                             114 SWY----YNNIRKNTS-----
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SOFTWARE: Patentin version 3.3
SEQ ID NO 171
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Best Local Similarity
                                     Best Local Similarity
Matches 40; Conserv
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US-11-087-099-10263
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APPLICANT: Steward, Lance E.
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                                                                                                                                                                            APPLICANT: Sutton, J. Mark
APPLICANT: Stancombe, Patrick
APPLICANT: Wayne, Jonathan
TITLE OF INVENTION: Recombinant Toxin Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Amino acid segence of HC US-10-909-769-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/255,829
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/782,893
PRIOR PILING DATE: 1956-12-27
PRIOR PILING DATE: 1956-12-13
PRIOR PILING DATE: 1956-12-13
PRIOR FILING DATE: 1956-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/077,550
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 10/241,596
PRIOR FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KIIKLIRTSNSNNSLGQIIVMDSIGNNC--
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Publication No. US20060024331A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 179
SOFTWARE: PatentIn version 3.1
SEQ ID NO 141
LENGTH: 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Clostridium tetani
US-11-077-550-141
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 1581.0130004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 40; Conserv
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